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OM nucleic - nucleic search, using sw model

Run on: July 17, 2002, 06:42:50 ; Search time 268.17 Seconds
(without alignments)
3418.847 Million cell updates/sec

Title: US-09-801-115-1

Perfect score: 534
Sequence: 1 gttcccaatcgaatgaag.....aaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
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10: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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13: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
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19: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	534	100.0	534	AAA38006	UCK-1 nucleotide s
2	507	94.9	655	AA544932	cdna encoding nove
3	498.2	93.3	538	AAH98515	Human EST-derived
4	498.2	93.3	538	AAH98548	Human EST-derived
5	497.2	93.1	558	AAH34835	Human colon cancer
6	493.4	92.4	515	AAH87730	Human secreted pro
7	493.4	92.4	515	AAH64012	cdna encoding huma
8	486.6	91.1	506	AAV59598	Human secreted pro
9	478.6	89.6	506	AAV59746	Human secreted pro

10	466.8	87.4	500	20	AA97826	Human secreted pro
11	465.4	87.2	467	21	AA15973	Human protein clon
12	461.4	77.0	413	20	AA97873	Human secreted pro
13	405.4	75.9	415	21	AAC00147	Human secreted pro
14	335	62.7	663	20	AA234051	Human PRO772 nucle
15	335	62.7	663	21	AAC78498	Human PRO772 nucle
16	335	62.7	663	21	AAC58238	Human PRO772 nucle
17	327.2	61.3	608	22	AA544933	cdna encoding nove
18	321.8	60.3	669	21	AAH87771	Human secreted pro
19	321.8	60.3	669	22	AAH64055	cdna encoding huma
20	309.8	58.0	354	20	AAH41509	Human secreted pro
21	309	57.9	637	21	AAZ56747	Human transmembran
22	300	56.2	566	22	AA545120	cdna encoding nove
23	300	56.2	566	22	AA545121	cdna encoding nove
24	295.4	55.3	392	21	AAH15919	Human protein clon
25	272	50.9	392	21	AAH16090	Human colon cancer
26	224.4	42.0	459	21	AAH38007	UCK-2 nucleotide s
27	214.4	40.1	6021	22	AAK82407	Human immune/haema
28	214.4	40.1	13744	22	AAK82406	Human immune/haema
29	214.4	40.1	13744	22	AAK82405	Human secreted pro
30	214	39.4	269	21	AAH97651	Extended human sec
31	210.2	39.4	321	20	AA234052	Human EST DNA43509
32	185.2	34.7	495	20	AA234051	cdna encoding spr
33	185.2	34.7	495	21	AAH78489	Human immune/haema
34	185.2	34.7	495	22	AAH93358	Human immune/haema
35	184.8	34.6	2953	22	AAK68359	Human secreted exp
36	184.8	34.6	2953	22	AAK68360	Human transmembran
37	178.8	33.5	379	21	AAH41312	Human gene regulat
38	160.8	30.1	465	22	AAH09082	UCK-4 nucleotide s
39	158.4	29.7	6283	24	AA561352	UCK-3 nucleotide s
40	130.6	24.5	363	21	AAH38009	Human gene regulat
41	127	23.8	204	21	AAH38008	Human EST-derived
42	119.4	22.4	6283	24	AAH61351	Human EST-derived
43	102.2	19.1	948	22	AAH98012	Human EST-derived
44	78.4	14.7	844	22	AAH98802	Human EST-derived
45	78.4	14.7	66566	21	AAH53450	Human thiredoxin

ALIGNMENTS

RESULT 1	
AAA38006	AAA38006 standard; cdna: 534 BP.
AAA38006:	
22-AUG-2000	(first entry)
XX	
AC	
XX	
DE	
XX	
XX	
KW	UCK-1: chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;
XX	radiotherapy; chemotherapy; human; ss.
OS	Homo sapiens.
XX	
PN	CN1244584-A.
XX	
PD	16-FEB-2000.
XX	
PF	14-MAY-1999; 99CN-0107284.
XX	
PR	14-MAY-1999; 99CN-0107284.
XX	
PA	(UYBE-) UNIV BEIJING MEDICAL.
XX	
PI	Ma D, Han W, Zhang Y;
XX	
DR	WPI: 2000-388170/34.
XX	P-PSDB: AAH98142.
PT	Chemotactic factor useful for treatment and diagnosis of immunocyte disorders - has immunocyte chemotactic stimulating factor


```

OY 19 agccgaagctggcagagaagtaaggagagcggtgctccgcgcggtggcggtgtgtatcg 78
DB 1 agccgaagctggcagagaagtaaggagagcggtgctccgcgcggtggcggtgtgtatcg 60
OY 79 ctccgagaacactcactcagaagcagcctgagaagaagttgaaggaagttctgctcg 138
DB 61 ctccgagaacactcactcagaagcagcctgagaagaagttgaaggaagttctgctcg 120
OY 139 gctcgcagacgcagtgatagacgtgacgcggaataaataacatgcgcctctgctcg 198
DB 121 gctcgcagacgcagtgatagacgtgacgcggaataaataacatgcgcctctgctcg 180
OY 199 tctgaagagccagctgaagatgctgcgcgctgagatattacacactcagtgtaaacag 258
DB 181 tctgaagagccagctgaagatgctgcgcgctgagatattacacactcagtgtaaacag 240
OY 259 attcattgctcgtatcgtgtgctgacgtgataccagaacacacacattgacagttgg 318
DB 241 attcattgctcgtatcgtgtgctgacgtgataccagaacacacacattgacagttgg 300
OY 319 tggagaggtgtgttgcactgtgacagcagatgctgcttgcgcgaggggcctattta 378
DB 301 tggagaggtgtgttgcactgtgacagcagatgctgcttgcgcgaggggcctattta 360
OY 379 ccggaagcttctgtcactccacagcgtccttaccagaanaagcctgtgcatgtaaaaaa 438
DB 361 ccggaagcttctgtcactccacagcgtccttaccagaanaagcctgtgcatgtaaaaaa 420
OY 439 agaaagtttgaatttatattactttagttgatactaatgataatttaacatttctg 498
DB 421 agaaagtttgaatttatattactttagttgatactaatgataatttaacatttctg 480
OY 499 tattcttccaaaaaataaaaaa 525
DB 481 tattcttccaaaaaataaaaaa 507

RESULT 3
AAH98515/c
ID AAH98515 standard; cDNA; 538 BP.
AC AAH98515;
DE 12-OCT-2001 (first entry)
XX Human EST-derived coding sequence SEQ ID NO: 372.
XX Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KM diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX Homo sapiens.
XX WO200154477-A2.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US02687.
XX 25-JAN-2000; 2000US-0491404.
XX 17-JUL-2000; 2000US-0617746.
XX 03-AUG-2000; 2000US-0631451.
XX 15-SEP-2000; 2000US-0663870.
XX (HYSE-) HYSEQ INC.
XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RB, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
XX P-PSDB; AAM23856.

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XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX Claim 1; Page 451; 1275pp; English.
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.
XX Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;
XX
XX Query Match 93.3%; Score 498.2; DB 22; Length 538;
XX Best Local Similarity 99.4%; Pred. No. 2; 1e-99;
XX Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 15 gtaagacgcagctggcagagaagtaaggagagcggtgctccgcgcggtggcggtgtgt 74
DB 503 GGAAGCCGAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444
OY 75 atgccttcgcagacactcactcagcagcagcagcagcagcagcagcagcagcagcagc 134
DB 443 ATGCTTTCGAGAACCTACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 384
OY 135 ctgggtctcagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 194
DB 383 CTGGGCTCGCAGACGCGATGATACGTCAGCCGAAATTAACATCCTCCCTTCCTGCT 324
OY 195 tcaaggtgaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 254
DB 323 TCAGTGTAAAGGCCACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 264
OY 255 caglatatcgtcactcgtatcgtgtgacacagcagcagcagcagcagcagcagcagcag 314
DB 263 CAGTATTCATGCTCATGCTATCTGTTGTCACATGATCCAGAAACCAACATTTGACAG 204
OY 315 ttgggtggaggggtgttgcactgtgacagcagcagcagcagcagcagcagcagcagc 374
DB 203 TTGGTGGAGGGGTGTTGCTACCTTGTGACAGCAGTATGCTGCTCCGACGGGGCCCTTA 144
OY 375 ttaccggaagcttctgtcactcagcagcagcagcagcagcagcagcagcagcagcagc 434
DB 143 TTACCGGAAGCTTGTCTCAATCCAGCGCTCTTACCAAGAAAGCCTGTGATGAAA 84
OY 435 aaaaagaagtttgaatttatattactttagttgatactaatgataatttaacatatt 494
DB 83 AAAAAGAGTTTGTATTTTATATTCTTTTATTTAGTTTATCTAAGTATTAACATATT 24
OY 495 tctgtatcttccaaaaaataaaaaa 517
DB 23 TCTGTATTCTTAAAAAATAAAAAA 1
XX
XX RESULT 4
XX AAH98548/c
XX ID AAH98548 standard; cDNA; 538 BP.
XX AC AAH98548;
XX DE 12-OCT-2001 (first entry)
XX Human EST-derived coding sequence SEQ ID NO: 405.
XX Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KM diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.

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XX Homo sapiens.
 OS
 XX
 PN WO200154477-A2.
 XX
 PD 02-AUG-2001.
 XX
 PE 25-JAN-2001; 2001WO-US02687.
 XX
 PR 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 DR MPI: 2001-476164/51.
 DR P-PSDB; AAM23889.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 XX antibodies and research use -
 PS Claim 1: Page 467; 1275pp; English.
 CC
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention.
 XX
 SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

Query Match 93.3%; Score 498.2; DB 22; Length 538;
 Best Local Similarity 99.4%; Pred. No. 2,1e-99;
 Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 gtgaagccgagctggcgaggaagtagggagggcggtgctccgcgagtgagttct 74
 DB 503 GGGAGCGCGAGCTGGCGAGGAAGTAGGGAGCGCGTCTCGCGCGGTGGCTTCT 444
 QY 75 atcgccttcgaggaactcagcagcagcagcagcagcagcagcagcagcagcagc 134
 DB 443 ATGCTTCGCGAGACCTACTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 384
 QY 135 ctgggtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 194
 DB 383 CTGGGCTTGGAGAGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
 QY 195 tcaagtgtgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 254
 DB 323 TCAGTGTGAAGAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 264
 QY 255 cagatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 314
 DB 263 CAGTATTCATGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
 QY 315 ttggtagaggggtgttggactgtgtacagcagcagcagcagcagcagcagcagcagcagcagc 374
 DB 203 TTGGTGAAGGGGTTTGGACTTGTGACAGCACTATGCTGCTTGGACGGGGCCCTTA 144
 QY 375 tttaacggaagcttctgtcaatccacagcagcagcagcagcagcagcagcagcagcagcagcagc 434
 DB 143 TTTACCGGAAGCTTCTGTCAATCCACAGCGGCTCTTAACAGAAAAAGCCTGTGCATGAAA 84
 QY 435 aaaagaagtttgaatttatattactttttagttgatactaagtttaaacattt 494

DB 83 AAAAAGAGCTTTGTAATTTATATTACTTTTGTGATGATGATGATGATGATGATGATGATGAT 24
 QY 495 tctgtatctctcccaaaaaaaaaa 517
 DB 23 TCTGTATCTCTTAAAAA 1

RESULT 5
 AAH34835
 ID AAH34835 standard; cDNA; 558 BP.
 XX
 AC AAH34835;
 XX

DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1917.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; ss.
 XX

OS Homo sapiens.
 XX
 PN WO200122920-A2.
 PD 05-APR-2001.
 XX

PF 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 PI WPI: 2001-235357/24.
 DR P-PSDB; AAG75430.
 XX

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 PS Claim 1: Page 3428; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC diagnosis and vaccine production. N and P may be used in the prevention,
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated P,
 CC to express the nucleic acids into a host cell and culturing the cell
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH3204
 CC and AAH7789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX

Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;

Query Match 93.1%; Score 497.2; DB 22; Length 558;
 Best Local Similarity 98.4%; Pred. No. 3.6e-99;
 Matches 499; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 tgaagcgaagcttggcgaggaagtagggagggcggtcgcgcgagggcggtgtgcta 75
 DB 11 tgaagysgagctgcgcgaggaagtagggagggcggtcgcgcgagggcggtgtgcta 70

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OY 76 tcgcttcgcaaacctactcagcagccagctggaagattgaggaaagtgcctgc 135
DB 71 tcgcttcgcaaacctactcagcagccagctggaagattgaggaaagtgcctgc 130
OY 136 tgggtctgcagacgcgattgatacgcctcagccgaaataaacaatgccttcgt 195
DB 131 tgggtctgcagacgcgattgatacgcctcagccgaaataaacaatgccttcgt 190
OY 196 cagctgtgaaaagccagcgtgaagatgctgcggctggaatataatcaactcgtgaacac 255
DB 191 cagctgtgaaaagccagcgtgaagatgctgcggctggaatataatcaactcgtgaacac 250
OY 256 agtattatgcctacgtatctgtgtgtgcactgataaccagaaacacacattacac 315
DB 251 agtattatgcctacgtatctgtgtgtgcactgataaccagaaacacacattacac 310
OY 316 tgggtgaggggtgtttgtaactgtgacagcaatgctgtctgcgacgagggcccttat 375
DB 311 tgggtgaggggtgtttgtaactgtgacagcaatgctgtctgcgacgagggcccttat 370
OY 376 ttaccggaagctctgttcaatccaccagcggtcccttaaccagaaagcctgtgcataa 435
DB 371 ttaccggaagctctgttcaatccaccagcggtcccttaaccagaaagcctgtgcataa 430
OY 436 aaaaagaagtttgaatttatattatatttgaatttgaattatataacataatt 495
DB 431 aaaaagaagtttgaatttatattatatttgaatttgaattatataacataatt 490
OY 496 ctgtattcttccaaaaaanaaaaaa 522
DB 491 ctgtattcttccaaaaaanaaaaaa 517

RESULT 6
AAA87730
ID AAA87730 standard; cDNA; 515 BP.
XX
AC AAA87730;
XX
DT 28-NOV-2000 (first entry)
XX
DE Human secreted protein encoding cDNA SEQ ID #29.
XX
KW Human; secreted protein; forensic procedure; gene therapy;
KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
KW brain disorder; skeletal muscle disorder; eye disorder; obesity;
KW mitochondrialopathy; diabetes; atherosclerosis; Alzheimer's disease;
KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
KW septic shock; impotence; ss.
XX
XX Homo sapiens.
XX
OS WO200037491-A2.
XX
PN 29-JUN-2000.
XX
PD 20-DEC-1999; 99WO-IB02058.
XX
PE 22-DEC-1998; 98US-0113686.
XX
PR 25-JUN-1999; 99US-0141032.
XX
XX (GENSET) GENSET.
XX
PI Bougueleret L, Dumas J, Duclert A.
XX
DR WPI: 2000-442637/38.
XX
DR P-PSDB; AAB25768.
XX
PT Polynucleotides and polypeptides encoding proteins with signal
PT peptides, useful in diagnostic, forensic, gene therapy and chromosome
PT mapping procedures -

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XX
PS Claim 1; Page 169-170; 306pp; English.
XX
CC This sequence represents human cDNA encoding a secreted protein. The
CC invention relates to sequences AAA87725-A87774 which encode human
CC secreted proteins AAB25763-B25812. The proteins include signal peptides.
CC Included in the invention are a host cell containing one of the cDNA
CC sequences, and a purified antibody capable of binding to one of the
CC secreted proteins. Also contained in the invention are methods for
CC storing the sequence data on a computer system, and a method for
CC identifying features of the cDNA sequences using a computer programme.
CC The cDNAs are useful for expressing secreted proteins or fragments to
CC obtain antibodies capable of specifically binding to the secreted
CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene
CC therapy and chromosome mapping procedures and may be used to design
CC expression vectors and secretion vectors. The proteins of the invention
CC may be used to treat diseases including cancer, autoimmune diseases,
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
CC disorders, obesity, mitochondrialopathies, diabetes, atherosclerosis,
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,
CC dementia, hyperlipidaemia, septic shock and impotence.
XX
SQ Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

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Query Match          92.4%; Score 493.4; DB 21; Length 515;
Best Local Similarity 99.4%; Pred. No. 2.4e-98;
Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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OY 15 gtaagccgagctggcgagaaagtaaggagggcggtgtcgcgcgcggtgtgcgt 74
DB 8 gggaagccgagctggcgagaaagtaaggagggcggtgtcgcg-cgcggtgtgcggtgt 66
OY 75 atcgtctgcagaaactactcactcagcagccagctgagaagaagttgagggaagtcgtc 134
DB 67 atcgtctgcagaaactactcactcagcagccagctgagaagaagttgagggaagtcgtc 126
OY 135 ctggtctgcagacgcgattgatacgtgacgacgcgaataaataacatcgcccttcgt 194
DB 127 ctggtctgcagacgcgattgatacgtgacgacgcgaataaataacatcgcccttcgt 186
OY 195 tcaagtgtgaagccacgtgaagatgctgcgctggaattatatacactcactgttaaca 254
DB 187 tcaagtgtgaagccacgtgaagatgctgcgctggaattatatacactcactgttaaca 246
OY 255 cagtatcatgcctcatcgtatctgtgtgacgtatatacagaagaacacacattgacg 314
DB 247 cagtatcatgcctcatcgtatctgtgtgacgtatatacagaagaacacacattgacg 306
OY 315 ttgtgaggggtgttgcacttgacagcagatgctgtcttgcgcaggggcctta 374
DB 307 ttgtgaggggtgttgcacttgacagcagatgctgtcttgcgcaggggcctta 366
OY 375 ttaccggaagctctgttaatccagcggtcccttaaccagaaagcctgtgataaa 434
DB 367 ttaccggaagctctgttaatccagcggtcccttaaccagaaagcctgtgataaa 426
OY 435 aaaaagaagtttgaattatatactttagattgatacgaattataacataatt 494
DB 427 aaaaagaagtttgaattatatactttagattgatacgaattataacataatt 486
OY 495 tctgtattcttccaaaaaanaaaaaa 522
DB 487 tctgtattcttccaaaaaanaaaaaa 514

RESULT 7
AAF64012
ID AAF64012 standard; cDNA; 515 BP.
XX
AC AAF64012;
XX

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PR 23-MAY-1997; 97US-0047595.
 PR 23-MAY-1997; 97US-0047596.
 PR 23-MAY-1997; 97US-0047597.
 PR 23-MAY-1997; 97US-0047598.
 PR 23-MAY-1997; 97US-0047599.
 PR 23-MAY-1997; 97US-0047600.
 PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.
 PR 13-JUN-1997; 97US-0051926.
 PR 08-JUL-1997; 97US-0052874.
 PR 16-JUL-1997; 97US-0055724.
 PR 18-AUG-1997; 97US-0056630.
 PR 22-AUG-1997; 97US-0056631.
 PR 22-AUG-1997; 97US-0056632.
 PR 22-AUG-1997; 97US-0056636.
 PR 22-AUG-1997; 97US-0056637.
 PR 22-AUG-1997; 97US-0056662.
 PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056864.
 PR 22-AUG-1997; 97US-0056872.
 PR 22-AUG-1997; 97US-0056874.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057659.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 PR XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
 PI Peng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
 PI Kyan H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX
 DR WPI; 1998-506364/43.
 DR P-PSDB; AAW74818.
 XX
 XX New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX

PS Claim 1; Page 320; 721bp; English.
 XX
 CC This sequence represents a nucleic acid molecule designated Gene 88 from
 CC the human cDNA clone HAUAV32 (deposited as clone ATCC 97901 and ATCC
 CC 209047) which encodes a secreted human protein. The gene can be used to
 CC generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-v59812; amino acid sequences AAW74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological conditions
 CC can be diagnosed by determining the presence of mutations in the new
 CC sample or by determining the presence of mutations in the new 186
 CC polynucleotides. Specific uses are described for each of the new 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).
 XX
 SQ Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;

Query Match 91.1%; Score 486.6; DB 19; Length 504;
 Best Local Similarity 99.0%; Pred. No. 7; 1e-97;
 Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 21 ccgagctggcgagaaagtgggagggcggtctccgcgcggtggcggtgtatcgcgt 80
 DB 1 ccgagctggcgagaaagtgggagggcggtctccgcgcggtggcggtgtatcgcgt 59
 QY 81 tcgcaaacctactctggcgagcgagctggaagaagtgtgaaggaaagtgtcgtctgggt 140
 DB 60 tcgcaaacctactctggcgagcgagctggaagaagtgtgaaggaaagtgtcgtctgggt 119
 QY 141 ctgcagacgcatgagataacgtggaacgcgaataaataacatcgcccttctgttcagtg 200
 DB 120 ctgcagacgcatgagataacgtggaacgcgaataaataacatcgcccttctgttcagtg 179
 QY 201 tgaagagccacgtgaagaatgtctgggtgataatatacaactcactgttaacaacagtat 260
 DB 180 tgaagagccacgtgaagaatgtctgggtgataatatacaactcactgttaacaacagtat 239
 QY 261 tcatgcatcactctcgtgtgtgtgacatgataccagaacacacacatgtgcaatgttg 320
 DB 240 tcatgcatcactctcgtgtgtgtgacatgataccagaacacacacatgtgcaatgttg 299
 QY 321 gaggggtgtttgacatgtgacagcagatctgtctgcgcagcgagggccctattacc 380
 DB 300 gaggggtgtttgacatgtgacagcagatctgtctgcgcagcgagggccctattacc 359
 QY 381 ggaagctctcttcaatccacagcgttccctaacagaanaagcctgtgcatgaaaaaaag 440
 DB 360 ggaagctctcttcaatccacagcgttccctaacagaanaagcctgtgcatgaaaaaaag 419
 QY 441 aagtttgtaatttatatactatttttagtttgatactgaatttaaaatattctgtga 500
 DB 420 aagtttgtaatttatatactatttttagtttgatactgaatttaaaatattctgtga 479
 QY 501 ttcttccaaaaaaataaaaaaa 525
 DB 480 ttcttccaaaaaaataaaaaaa 504

RESULT 9
 AAV59746
 ID AAV59746 standard; DNA; 506 BP.
 AC AAV59746;
 XX
 XX 19-JAN-1999 (first entry)
 DT
 XX
 XX Human secreted protein gene 88 clone HAUAV32.
 DE
 XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW

DT 07-DEC-1999 (first entry)
 XX Human PRO772 nucleotide sequence.
 XX Human: PRO: EST: expressed sequence tag; PCR primer; hybridisation;
 KM probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KM secreted protein; transmembrane protein; ss.
 XX Homo sapiens.
 PN MO9946281-A2.
 PD 16-SEP-1999.
 XX 08-MAR-1999; 99WO-US05028.
 PF 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077791.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 25-MAR-1998; 98US-0078939.
 PR 26-MAR-1998; 98US-0079294.
 PR 27-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
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 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081955.
 PR 15-APR-1998; 98US-0081957.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.
 PR 28-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.

PR 05-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085597.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100036.
 XX (GETH) GENENTECH INC.
 PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX WPI; 1999-551358/46.
 FI P-PSDB; AAY41713.
 XX New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders -
 XX
 XX
 PS Claim 2; Fig 69; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AA33891 to
 CC AA33338, and AAY41685 to AAY41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 663 BP; 180 A; 137 C; 153 G; 193 T; 0 other;

Query Match 62.7%; Score 335; DB 20; Length 663;
 Best Local Similarity 76.0%; Pred. No. 7.4e-64;
 Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

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 QY 82 cgcagaacctactcagcagcaagcagctgagagaggttgaagggaagtctctgtggtc 141
 Db 61 cgcagaacctactcagcagcagcagctgagagaggttgaagggaagtctctgtggtc 120
 QY 142 tgcagagcgcgagtgtgataacgttcagcccgaaataaataacatgcgcccttcgtcagtg 201


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Db 421 ggcactgataccagaacacacacatgacagttggtgaggggtgttgcactgtgac 480
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Db 481 agcagtatgtctgtcttgcgcgagcgccctatttaccggaagcttctgttcaatccag 540
QY 403 cggctcctaacgagaagcctgtgcatgaaaaaagaagtttctaattatattac 462
Db 541 cggctcctaacgagaagcctgtgcatgaaaaaagaagtttctaattatattac 600
QY 463 ttittagttgatactagtttaacatatcttctgtatcttccaaaaaataaaaaa 522
Db 601 ttittagttgatactagtttaacatatcttctgtatcttccaaaaaataaaaaa 660
QY 523 aaa 525
Db 661 aaa 663

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 Job time: 9644 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 17, 2002, 07:02:45 ; Search time 77.95 Seconds
(without alignments)
1682.723 Million cell updates/sec

Title: US-09-801-115-1
Sequence: 534
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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27.2	50.9	392	US-09-385-982-95	Sequence 95, Appl
2	50.4	9.4	1582	US-08-545-196B-10	Sequence 10, Appl
3	50.4	9.4	1582	US-08-545-196B-12	Sequence 12, Appl
4	46.8	8.8	770	US-08-865-297-5	Sequence 5, Appl
5	45.8	8.6	3761	US-08-890-865A-2	Sequence 2, Appl
6	45	8.4	961	5194596-16	Patent No. 5194596
7	45	8.4	5219739-16	Sequence 1, Appl	Sequence 1, Appl
8	44.6	8.4	2920	US-09-276-400-1	Sequence 35, Appl
9	44.6	8.3	333	US-08-946-026-35	Sequence 22, Appl
10	44.2	8.3	381	US-08-557-309B-22	Sequence 22, Appl
11	44.2	8.3	581	US-08-834-306-22	Sequence 22, Appl
12	44.2	8.3	581	US-08-993-674A-22	Sequence 1, Appl
13	43	8.1	2589	US-08-569-749-1	Sequence 1, Appl
14	43	8.1	2589	PCT-US96-12860-1	Sequence 5, Appl
15	43	8.1	3238	US-08-123-934A-5	Sequence 1, Appl
16	43	8.1	3238	PCT-US94-10080-5	Sequence 1, Appl
17	42.8	8.0	1332	US-09-057-762-1	Sequence 1, Appl
18	42.8	8.0	1332	US-08-326-119A-1	Sequence 2, Appl
19	42.8	8.0	3471	PCT-US93-00227-2	Sequence 12, Appl
20	42.8	8.0	940	US-08-471-717-1	Sequence 12, Appl
21	41.8	7.9	742	US-07-847-010-12	Sequence 2, Appl
22	41.4	7.8	5852	US-07-867-106-2	Patent No. 5168051
23	41.4	7.7	2671	US-08-801-9	Sequence 3, Appl
24	41.2	7.7	3459	US-08-980-060-3	Sequence 3, Appl
25	41.2	7.7	3459	US-09-307-185-3	Sequence 4, Appl
26	41.2	7.6	1046	US-08-361-467B-4	Sequence 4, Appl
27	40.8	7.6			

28	40.8	7.6	1046	US-08-484-332C-4	Sequence 4, Appl
29	40.6	7.6	731	US-08-451-405A-2	Sequence 2, Appl
30	40.6	7.6	2444	US-08-906-791-1	Sequence 18, Appl
31	40.6	7.6	2625	US-09-245-041-18	Sequence 1, Appl
32	40.4	7.6	1253	US-08-591-629-1	Sequence 10, Appl
33	40.4	7.6	1472	US-08-781-420-10	Sequence 12, Appl
34	40.4	7.6	1472	US-08-781-420-12	Sequence 12, Appl
35	40.4	7.6	1472	US-08-874-102-10	Sequence 12, Appl
36	40.4	7.6	1472	US-08-874-102-12	Sequence 12, Appl
37	40.4	7.6	1472	US-08-874-102-16	Sequence 12, Appl
38	40.4	7.6	1881	US-08-874-102-48	Sequence 46, Appl
39	40.4	7.6	2007	US-08-747-221B-36	Sequence 38, Appl
40	40.4	7.6	2007	US-08-747-221B-38	Sequence 38, Appl
41	40.4	7.6	2007	US-09-005-051-36	Sequence 38, Appl
42	40.4	7.6	2007	US-09-005-051-38	Sequence 38, Appl
43	40.4	7.6	2217	US-09-244-314-1	Sequence 542, Appl
44	40.2	7.5	770	US-09-385-982-542	Sequence 1, Appl
45	40.2	7.5	817	US-08-885-469-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-385-982-95
Sequence 95, Application US/09385982
Patent No. 6262334
GENERAL INFORMATION:
APPLICANT: ENDERGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCNDA-260XX US/09/385, 982
CURRENT FILING DATE: 1999-08-30
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117, 393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098, 639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 344
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 95
LENGTH: 392
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(392)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-95

Query Match 50.9%; Score 27.2; DB 4; Length 392;
Best Local Similarity 95.5%; Pred. No. 8.4e-61;
Matches 297; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY	226	gctgatatataatcaatcgtgtacacagatattcatgcatcgtatctgtgtgac	285
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QY	286	actgataccgaac	345
DB	103	actgataccgaac	162
QY	346	agtagtctgtctgcgagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	405
DB	163	agtagtctgtctgcgagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	222
QY	406	tccatcagaagaagcctgtgtcatg-aaaaaagaagctttgttaatttattact	464
DB	223	tccatcagaagaagcctgtgtcatgataaaaaagaagctttgttaatttattact	282

Oy 465 tt-agttgataactaataacatattctgtatcttccaaaaa 523
 Db 283 nttaagttgataactaataacatattctgtatcttccaaaaa 342
 Oy 524 aaaaaa 534
 Db 343 tnaantanaa 353

RESULT 2

US-08-545-196B-10
 ; Sequence 10, Application US/08545196B
 ; Patent No. 6080577
 ; GENERAL INFORMATION:
 ; APPLICANT: MELKI, JUDITH
 ; APPLICANT: MINNICH, ARNOLD
 ; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
 ; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 ; STREET: PO BOX 747
 ; CITY: FALLS CHURCH
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/545,196B
 ; FILING DATE: 19-OCT-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FARACI, C. J.
 ; REGISTRATION NUMBER: 32,350
 ; REFERENCE/DOCKET NUMBER: 2121-110P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 205-8000
 ; TELEFAX: (703) 205-8050
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1582 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; US-08-545-196B-10

Query Match 9.4%; Score 50.4; DB 3; Length 1582;
 Best Local Similarity 71.7%; Pred. No. 0.0006;
 Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Oy 443 gtttgtaatttatattacttttgaattgataactaataacatattctgtat 502
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 Oy 503 ctcccaaaaaa 534
 Db 1487 ttttaaaaaa 1518

RESULT 3

US-08-545-196B-12
 ; Sequence 12, Application US/08545196B
 ; Patent No. 6080577
 ; GENERAL INFORMATION:
 ; APPLICANT: MELKI, JUDITH
 ; APPLICANT: MINNICH, ARNOLD
 ; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE

;; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
 ;; NUMBER OF SEQUENCES: 65
 ;; CORRESPONDENCE ADDRESS:
 ;; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 ;; STREET: PO BOX 747
 ;; CITY: FALLS CHURCH
 ;; STATE: VA
 ;; COUNTRY: USA
 ;; ZIP: 22040-0747
 ;; COMPUTER READABLE FORM:
 ;; MEDIUM TYPE: FLOPPY disk
 ;; OPERATING SYSTEM: IBM PC compatible
 ;; SOFTWARE: Patentin Release #1.0, Version #1.30
 ;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/08/545,196B
 ;; FILING DATE: 19-OCT-1995
 ;; CLASSIFICATION: 435
 ;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: FARACI, C. J.
 ;; REGISTRATION NUMBER: 32,350
 ;; REFERENCE/DOCKET NUMBER: 2121-110P
 ;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: (703) 205-8000
 ;; TELEFAX: (703) 205-8050
 ;; INFORMATION FOR SEQ ID NO: 12:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 1582 base pairs
 ;; TYPE: nucleic acid
 ;; STRANDEDNESS: double
 ;; TOPOLOGY: linear
 ;; MOLECULE TYPE: CDNA
 ;; US-08-545-196B-12

Query Match 9.4%; Score 50.4; DB 3; Length 1582;
 Best Local Similarity 71.7%; Pred. No. 0.0006;
 Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Oy 443 gtttgtaatttatattacttttgaattgataactaataacatattctgtat 502
 Db 1427 gtttgtaatttatattacttttgaattgataactaataacatattctgtat 502
 Oy 503 ctcccaaaaaa 534
 Db 1487 ttttaaaaaa 1518

RESULT 4

US-08-865-297-5
 ; Sequence 5, Application US/08865297
 ; Patent No. 6010853
 ; GENERAL INFORMATION:
 ; APPLICANT: Prasad V. S. Kanteti, Zhaochui Ao, and Stuart F.
 ; APPLICANT: Schlusman
 ; TITLE OF INVENTION: The Siva Genes, No. 6010853el Genes Involved in
 ; TITLE OF INVENTION: C027-mediated Apoptosis
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/865,297
 ; FILING DATE: 29-MAY-1997

RESULT 7
5219739-16
Patent No. 5219739
Applicant: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,
JOHN C.; MITCHELL, RICHARD I.
TITLE OF INVENTION: DNA SEQUENCES ENCODING BVGEF120 AND
HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
BVGEF120 AND METHODS FOR THE PRODUCTION OF BVGEF120 AND HVEGF121
NUMBER OF SEQUENCES: 40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/559,041
FILING DATE: 27-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 450,883
FILING DATE: 14-DEC-1989
APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
SEQ ID NO:16

LENGTH: 961
5219739-16

Query Match
Best Local Similarity 8.4%; Score 45; DB 6; Length 961;
Matches 69; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 426 tgcattgataaaagaagtttgtaatttatttacttttgaattgtaactgaatt 485
DB 852 tacatttatataatataatataatataatataatataatataatataatata 911
QY 486 aacataattctgtatcttcccaaaaaaaaaaaaaaaaaaaaaa 534
DB 912 tataataatataatattcttlttaaaaaaaaaaaaaaaaaaaaaa 960

RESULT 8
US-09-276-400-1

Sequence 1, Application US/09276400
Patent No. 6140056

GENERAL INFORMATION:

APPLICANT: Khodadoust, Mehran

TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND

FILE REFERENCE: MNI-073

CURRENT APPLICATION NUMBER: US/09/276,400

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 2920

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (143)..(2401)

US-09-276-400-1

Query Match
Best Local Similarity 8.4%; Score 44.6; DB 3; Length 2920;
Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 444 ttgttaatttatttacttttgaattgatactaaagtaacataattctgtatc 503
DB 2820 ttactataatagtgctgaggtataatttttataataaagtgcttctgtatc 2879
QY 504 ttccaaaaaataaaaaaaaaaaaaa 534
DB 2880 ctccagaaaaaataaaaaaaaaaaaaa 2910

RESULT 9
US-09-448-076-1

Sequence 1, Application US/09448076
Patent No. 6300092

GENERAL INFORMATION:

APPLICANT: Khodadoust, Mehran et al.

TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN

FILE REFERENCE: MNI-073CP

CURRENT APPLICATION NUMBER: US/09/448,076

EARLIER FILING DATE: 1999-11-23

EARLIER APPLICATION NUMBER: 60/117,580

EARLIER FILING DATE: 1999-01-27

EARLIER APPLICATION NUMBER: 09/276,400

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 2920

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS
LOCATION: (143)..(2401)
US-09-448-076-1

Query Match
Best Local Similarity 8.4%; Score 44.6; DB 4; Length 2920;
Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 444 ttgttaatttatttacttttgaattgatactaaagtaacataattctgtatc 503
DB 2820 ttactataatagtgctgaggtataatttttataataaagtgcttctgtatc 2879
QY 504 ttccaaaaaataaaaaaaaaaaaaa 534
DB 2880 ctccagaaaaaataaaaaaaaaaaaaa 2910

RESULT 10
US-09-946-026-35

Sequence 35, Application US/08946026
Patent No. 6034218

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Dillon, Davin G.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Mitcham, Jennifer L.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESS: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/946,026

FILING DATE: 07-Oct-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kaki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.424C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 333 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-946-026-35

Query Match
Best Local Similarity 8.3%; Score 44.4; DB 3; Length 333;
Matches 63; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 441 aagtttgtaatttatttacttttgaattgatactaaagtaacataattctgtatc 500
DB 233 AACTTGAATATATGTTGCCAATCTCTTTTCTTAATGAATTAATGTTTATATA 292
QY 501 ttcttcaaaaaaaaaaaaaaaaaaaaaa 534

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-993-674A-22

Query Match 8.3%; Score 44.2; DB 4; Length 581;
Best Local Similarity 68.5%; Pred. No. 0.015;
Matches 61; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 446 ttgtaatttattactttttagttgataactaataacataattctgtattctt 505
Db 484 ttttttttattgtcttttttttttttttttttttttttttttttttttttt 543
QY 506 ccaaaaaaaaaaaaaaaaaaaaaa 534
Db 544 CAAAAAAAAAAAAAAAAAAAAA 572

RESULT 14
US-08-569-749-1
Sequence 1, Application US/08569749
Patent No. 6187557

GENERAL INFORMATION:
APPLICANT: Roedel, Mike
APPLICANT: Goedel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
CLASSIFICATION:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-569-749-1

Query Match 8.1%; Score 43; DB 4; Length 2589;
Best Local Similarity 64.6%; Pred. No. 0.057;
Matches 64; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 436 aaaaagatttgytaattatattacttttagttgataactaagtaataacattt 495
Db 2468 AAAATAAGGATTTTCTCTATTCTCCCTAGTTGTGAGAAACATCTCAATAAAGTG 2527
QY 496 ctgtattcttcaaaaaaaaaaaaaaaaaaaaaa 534
Db 2528 CTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2566

RESULT 15
PCT-US96-12860-1
Sequence 1, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
CLASSIFICATION:
FILING DATE: 06 AUG 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US96-12860-1

Query Match 8.1%; Score 43; DB 5; Length 2589;
Best Local Similarity 64.6%; Pred. No. 0.057;
Matches 64; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 436 aaaaagatttgytaattatattacttttagttgataactaagtaataacattt 495
Db 2468 AAAATAAGGATTTTCTCTATTCTCCCTAGTTGTGAGAAACATCTCAATAAAGTG 2527
QY 496 ctgtattcttcaaaaaaaaaaaaaaaaaaaaaa 534
Db 2528 CTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2566

Search completed: July 17, 2002, 09:25:08
Job Time: 8543 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2002, 06:05:10 ; Search time 1859.31 Seconds
(without alignments)
6010.171 Million cell updates/sec

Title: US-09-801-115-1
534
Perfect score: 1 gttccacatcgaagtggaag.....aaaaaaaaaaaaaaaaaaaaa 534
Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_mu:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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1	518.4	97.1	530	9	AF096895
2	493.4	92.4	515	6	AX061624
3	349.4	65.4	689	9	AF135380
4	349	65.4	593	9	AF145216
5	338	63.3	688	9	BC004380
6	325.4	60.9	655	9	AF057306
7	321.8	60.3	669	6	AX061665
8	316.4	59.3	434	9	AF135381
9	278	52.1	485	11	G30204
10	214.4	40.1	97083	9	AC010289
11	214.4	40.1	151620	2	AC018589
12	214.4	40.1	188460	2	AC010542
13	205	38.4	207	6	AX330610
14	205	38.4	207	6	AX330787
15	205	38.4	207	6	AX331008
16	185.2	34.7	455	6	AX079435
17	184.8	34.6	189821	2	AC018557
18	165.4	31.0	523	10	AF253064
19	158.4	29.7	6283	6	AX252053
20	158.4	29.7	6283	6	AX344431
21	158.4	29.7	6283	6	AX348836
22	135	25.3	568	10	AY047360
23	126	23.6	6283	6	AX252052
24	119.4	22.4	6283	6	AX344430
25	119.4	22.4	6283	6	AX348835
26	119.4	22.4	6283	6	AC000090
27	78.4	14.7	4516	9	AY046597
28	63.8	11.9	527	10	BC008268
29	52.4	9.8	1926	10	BC018270
30	51.4	9.6	2699	10	BC018270
31	50.6	9.5	2165	9	BC009565
32	50.6	9.5	1525	9	BC015308
33	50.4	9.4	1525	6	A77033
34	50.4	9.4	1582	6	A77035
35	50.4	9.4	1582	6	AR100218
36	50.4	9.4	1582	6	AR100220
37	50.2	9.4	1597	3	DDPDEI
38	50.2	9.4	110000	2	PFMALAP1_2
39	50.2	9.4	2483	3	DDI13A
40	50	9.3	608	6	A31038
41	49.6	9.3	1345	10	BC011306
42	49.6	9.3	16344	2	AC006280
43	49.6	9.3	169794	2	AC004688
44	49.6	9.3	196149	2	AC004709
45	49.6	9.3	196149	2	AC004709

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE
1	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FLI-CDNA.	human.	Homo sapiens	530 bp	MRNA linear PRI 18-JUL-2001
	AF096895	Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.	AF096895	GI:9989691	FL				

TITLE Direct Submission
JOURNAL Submitted (03-OCT-1998) Immunology, Beijing Medical University, 38
REFERENCE Xue Yuan Rd., Beijing 100083, China
AUTHORS 3 (bases 1 to 530)
TITLE Han, W.L.
JOURNAL Direct Submission
REMARK Submitted (07-SEP-2000) Immunology, Peking University Health
COMMENT Science Center, Xueyuan Road 38, Beijing 100083, China
FEATURES Sequence update by submitter
On Sep 7, 2000 this sequence version replaced g1:628733.
source
Location/Qualifiers
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/cell_line="U937"
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1..530
/gene="CKLF1"
/note="CKLF1"
/note="GCK-1"
148..447
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/note="Increased expression in PHA stimulated cells;
expression inhibited by IL-10"
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/translation="MDNVPKIKHREPCFSVKGHVKNLRDIIINSLVTVPMILVSVL
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BASE COUNT 156 a 108 c 137 g 129 t

Query Match 97.1%; Score 518.4; DB 9; Length 530;
Best Local Similarity 99.8%; Pred. No. 2.3e-116;
Matches 519; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 75 atcgcttcgcaaacactactcaggcagcgagtggaagtgtagggaggaagtgctgctg 134
DB 71 ATCGCTTCGCAACCTACTACGACGCCAGCTGAGAAAGATTGAGGAAAGTGTCTGCTG 130
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DB 191 TCAGTGTGAAGGCGCAGTGAAGATGCTGCGGCTGGATATTATCACTCACTGTACAA 250
QY 255 cagatcactgcatatgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 314
DB 251 CAGTATTCATGCTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
QY 315 ttgggtgagggggtgtgtgctgctgctgctgctgctgctgctgctgctgctgctgctg 374
DB 311 TTGGTGGAGGGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
QY 375 tttaaccggaagctctgttcaatcccaagcggtctaccagaagaaagcctgtgcatgaa 434
DB 371 TTTAACGGGAAGCTTCTGTTCAATCCAGCGTCTTACCAAGAAAAGCCTGTGCTGAA 430
QY 435 aaaaagaagcttctgtaattatatactttttagttttagtacttaagtaatacatatt 494
DB 431 AAAAAAGAGTTTGTAAATTTTATTTACTTTTAACTTTTGAATTAAGTAATTAACATATT 490
QY 495 tctgctatcttccaaaaaataaaaaaataaaaaa 534
DB 491 TCTGATTTCTTCCAAAAAATAAAAAAATAAAAAA 530

RESULT 2
LOCUS AX061624
DEFINITION Sequence 29 from Patent WO0100806.
ACCESSION AX061624
VERSION AX061624.1 GI:12406709
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 515)
AUTHORS dumas milne Edwards, J.B., Bougueret, L. and Jobert, S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 29 04-Jan-2001;
GENSET (FR)
FEATURES Location/Qualifiers
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BASE COUNT 143 a 106 c 135 g 130 t 1 others
ORIGIN
Query Match 92.4%; Score 493.4; DB 6; Length 515;
Best Local Similarity 99.4%; Pred. No. 3e-110;
Matches 503; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 15 gtagagcgaagctggcgaggaagtagggagggcggtgctccgcgcggtgagtgctgct 74
DB 8 GGAAGCCGAGCTGGCGAGAGTAGGAGGCGGCTGCTCCGCGGCGGCTGCTGCT 66
QY 75 atcgcttcgcaaacactactcaggcagcgagtggaagtgtagggaggaagtgctgctg 134
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QY 135 ctgggtctgcagacgcatgatacgtgcaagccgaaataaacaatgcgcctctgctg 194
DB 127 CTGGGTCTGCAGACCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 186
QY 195 tcaatgtgaagcagcgtgaagatgctgctgctgctgctgctgctgctgctgctgctg 254
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QY 255 cagatcactgcatatgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 314
DB 247 CAGTATTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 306
QY 315 ttgggtgagggggtgtgtgctgctgctgctgctgctgctgctgctgctgctgctgctg 374
DB 307 TTGGTGGAGGGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
QY 375 tttaaccggaagctctgttcaatcccaagcggtctaccagaagaaagcctgtgcatgaa 434
DB 367 TTTAACGGGAAGCTTCTGTTCAATCCAGCGTCTTACCAAGAAAAGCCTGTGCTGAA 426
QY 435 aaaaagaagcttctgtaattatatactttttagttttagtacttaagtaatacatatt 494
DB 427 AAAAAAGAGTTTGTAAATTTTATTTACTTTTAACTTTTGAATTAAGTAATTAACATATT 486
QY 495 tctgctatcttccaaaaaataaaaaaataaaaaa 522

DB 487 TCGTATCTTCCAAAAA 514

RESULT 3
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LOCUS Homo sapiens chemokine-like factor 2 (CKLF2) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF135380
VERSION AF135380.2 GI:9989692
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 689)
AUTHORS Han, W.L., Gu, W., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.
JOURNAL Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
2 (bases 1 to 689)
REFERENCE Direct Submission
AUTHORS Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
JOURNAL Sequence update by submitter
REMARK On Sep 7, 2000 this sequence version replaced gi:6630853.
COMMENT Location/Qualifiers
FEATURES
Source
1..689
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148..606
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BASE COUNT 195 a 140 c 161 g 193 t
ORIGIN

Query Match 65.4%; Score 349.4; DB 9; Length 689;
Best Local Similarity 76.4%; Pred. No. 4.8e-75;
Matches 519; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

QY 15 gtgaagccagagctggcggaagaagagggcggtgctccgcccggcggtggtgctg 74
DB 11 gggaagccgagctggcggaagaagagggcggtgctccgcccggcggtggtgct 70
QY 75 atcgcttcgagaaacttaactgagcagccagctgaagaagagttgaggaagagtgctg 134
DB 71 atcgcttcgagaaacttaactgagcagccagctgaagaagagttgaggaagagtgctg 130
QY 135 ctggagcttcgagaaagctgtaactgagcagccagcgaataaataacatcgcccttctg 194
DB 131 ctggagcttcgagaaagctgtaactgagcagccagcgaataaataacatcgcccttctg 190
QY 195 tcagtgtaagaagccacgtgaagaatgctggcggtg 229
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QY 230 ----- 229

DB 251 TTTTATCATGCGACAGGCCCTGACCATATATTGTATCATCTGATTTGAGTACCG 310
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DB 311 TTATCTTATTTTCATACCTTTATATGATCTGACACTTGATGATTAATGAAGTGTAT 370
QY 230 -----gatattcaactcaactgtaacaacagattcatgctcatgcat 275
DB 371 TTGGCCCTTTCCTTGTATATCATCTGATCTGATTAATGAAGTGTAT 430
QY 276 ctggtgttcgactgatacagaacacacacacatgacagttggtgaggggtgttgac 335
DB 431 CTGTGTGGCAGCATGATACCAAGAACCAATGACAGTGGTGGAGGGGTGTGGAC 490
QY 336 ttgtgacagcagatgctgtcttcgagcaggggcccatttaccggaagcttcgttca 395
DB 491 TTGTGACAGCAGATGATGCTGTCTGCGACGGGGCCCTTATTTACCGGAACCTTCTGTCA 550
QY 396 atccacagcgtccttaccagaagaagcctgtgcatgtaaaaaaagaagtttgattt 455
DB 551 ATCCGACGGGCTCTTACACAGAAAAGCCTGTGCATGAAAAAGAAAGTTTGTATTTT 610
QY 456 atattacttttagtttgatgataagataacataattctgtattcttccaaaaaa 515
DB 611 ATATTACTTTTATGTTTATCTATAGTTTAAACATATTTCTGTATCTTCCAAAAA 670
QY 516 aaaaaaaaaaaaaaaaaa 534
DB 671 AAAAAAAAAAAAAAAAAA 689

RESULT 4
AF145216 593 bp mRNA linear PRI 07-SEP-2000
LOCUS Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF145216
VERSION AF145216.2 GI:9989694
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 593)
AUTHORS Han, W.L., Gu, W.F., Li, Y., Zhang, Y.M., Di, C.H., Song, Q.S. and
Ma, D.L.
JOURNAL Direct Submission
TITLE Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
2 (bases 1 to 593)
REFERENCE Direct Submission
AUTHORS Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
JOURNAL Sequence update by submitter
REMARK On Sep 7, 2000 this sequence version replaced gi:6625671.
COMMENT Location/Qualifiers
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1..593
/gene="CKLF4"
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148..510
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 373 TGATATTATCACTCACTCGTAAACACAGATCATCATCTCTATCTGTTGGACT 432
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 289 gatccagaacacacacatctgacagtctgttggagggtgtttgcaactctgacacagcagt 348

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Db	181	TGAAGGCCACGCTGAAGATGCTCGGCTGGCACTAACGTGACATCTATAGCCTTTT	240
Qy	230	-----	229
Db	241	TCATGCCACAGGCCCTGACACCATATATGTTATCACTGGATTGTAAGTCAACCGTTACT	300
Qy	230	-----	229
Db	301	TATTTTTCATACTTTTATATGTACTGACGCTTGATGATTAAGTGGTATTTTGGC	360
Qy	230	-----gatatacctaactactggtgaacaagaatattcagtcacatgatactgagt	281
Db	361	CTTTGCTTGATTTATTCACACTCACCTGGGTAAACAGATTTACATGCTCATCGTATCTGT	420
Qy	282	tggactgatatacgaaaaaccacaacatgacagttggtggaagggtgtttgcacattgta	341
Db	421	TGGCACTGTGATACAGAAACACACAAACATTGACAGTGTGGAGGGGTATTTGCACCTGTGA	480
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Db	481	CAGCAGATGCTGCTCTTTGGCGAGGGGGCCCTTATTTACCGGAGCTTCTGTTCATCCCA	540
Qy	402	gcgagctcttaccggaaaaagcctgltgcaltgaaaaaaaagaagcttttgyaaatttaatta	461
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Qy	462	ctttttagttgatactaagatattaacattctcgtatcttccnaaaaaa	516
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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 485)
JOURNAL Myers, R.M.
COMMENT Unpublished (1996)

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: ACTCTCTTTTTCATGCACAGC
Primer B: GCCCTATTACCGAAGCT
STS size: 77
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng
each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/uL
Total Vol: 10 uL

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T90569
-- Washington University/Merck EST sequence.

FEATURES

source

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ORIGIN

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Best Local Similarity 97.9%; Pred. No. 1.3e-57;
Matches 261; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 287 GCTTGATATATCAACACACACATGTAACACAGATATCATGCTCATCTGTAACCTGTTGGC 228

OY 286 acgataccagaaacacacacattgacagttggtggaagggtgttgcacttgcagacg 345

DB 227 ACTGATACCAAGAACCAACACATTGACAGTTGGGAGGGGCTGTTGCACTTGAGACAGC 168

OY 346 agtatagtctcttgcagcaggggcccattattaccggaagcttgcataatccacgag 405

DB 167 AGTATGCTGCTTCCGACGCGGCGCTTATTACCGAAGCTGTTCAATCCACGCG 108

OY 406 tccttaccagaaaagcgtgtgcctgtaaaaaaagaagtttgttaatttatattactt 465

DB 107 TCCTTACCAAGAAAGCCTGTGATGAAAAAAGAGTTTGTATTTTATTACTTT 48

OY 466 ttattgtactactaagatataacatattctgtatcttccaaaa 512
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RESULT 10
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LOCUS
DEFINITION Homo sapiens chromosome 16 clone CTA-989F12, complete sequence.
AC010289
AC010289.9 GI:15451657
VERSION
KEYWORDS
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
JOURNAL
TITLE
DOI Joint Genome Institute and Stanford Human Genome Center.

REFERENCE
AUTHORS
JOURNAL
TITLE
Unpublished

REFERENCE
AUTHORS
JOURNAL
TITLE
DOE Joint Genome Institute.

REFERENCE
AUTHORS
JOURNAL
TITLE
Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS
JOURNAL
TITLE
Direct Submission
Submitted (10-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS
JOURNAL
TITLE
Direct Submission
Submitted (09-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS
JOURNAL
TITLE
Direct Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Direct Submission
Submitted (10-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Direct Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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AUTHORS
JOURNAL
TITLE
Direct Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS
JOURNAL
TITLE
Direct Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS
JOURNAL
TITLE
Direct Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS
JOURNAL
TITLE
Direct Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

QY 303 caacattgacagtggtgaggggtgttgcactgtgacagcagatgctgtccg 362
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 Db 207 CAACATTGACAGTTGTGGAGGGGTGTGACTTGTACAGCAATAGCTGTCTGGCG 148
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 QY 363 acggggcccttattaccggaagcttctgtcaatccagcgggtccctaccagaaagc 422
 |||||||
 Db 147 ACGGGCCCTTATTATCCGGAAGCTTCTGTCAATCCAGCGGTCTTACAGNAAAGC 88
 |||||||
 QY 423 ctgtgcatagaanaaagaagtttgttaatttatattacttttagttgataactagt 482
 |||||||
 Db 87 CTGTGCATGAAAAAAGAGTTTGTATTTATTTACTTTTGTAGTTGATCTAAGT 28
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 QY 483 attaacatatcttctgtattctcca 508
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 Db 27 ATTAACATATTCTGTATTCTTCCA 2
 |||||||

RESULT 14
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 DEFINITION Sequence 1296 from Patent WO0194629.
 ACCESSION AX330787
 VERSION AX330787.1 GI:18103765
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (sites)
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
 gene sets
 Patent: WO 0194629-A 1296 13-DEC-2001;
 Avalon Pharmaceuticals (US)
 Location/Qualifiers
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 ORIGIN

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 Db 207 CAACATTGACAGTTGTGGAGGGGTGTGACTTGTACAGCAATAGCTGTCTGGCG 148
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 Db 87 CTGTGCATGAAAAAAGAGTTTGTATTTATTTACTTTTGTAGTTGATCTAAGT 28
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 QY 483 attaacatatcttctgtattctcca 508
 |||||||
 Db 27 ATTAACATATTCTGTATTCTTCCA 2
 |||||||

RESULT 15
 AX331008/C
 LOCUS AX331008 207 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 1517 from Patent WO0194629.
 ACCESSION AX331008
 VERSION AX331008.1 GI:18121642
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (sites)
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
 gene sets
 Patent: WO 0194629-A 1517 13-DEC-2001;
 Avalon Pharmaceuticals (US)
 Location/Qualifiers
 1. 207
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 70 a 43 c 39 g 54 t 1 others
 ORIGIN

Query Match 38.4%; Score 205; DB 6; Length 207;
 Best Local Similarity 99.5%; Pred. No. 7.3e-40;
 Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 303 caacattgacagtggtgaggggtgttgcactgtgacagcagatgctgtccg 362
 |||||||
 Db 207 CAACATTGACAGTTGTGGAGGGGTGTGACTTGTACAGCAATAGCTGTCTGGCG 148
 |||||||
 QY 363 acggggcccttattaccggaagcttctgtcaatccagcgggtccctaccagaaagc 422
 |||||||
 Db 147 ACGGGCCCTTATTATCCGGAAGCTTCTGTCAATCCAGCGGTCTTACAGNAAAGC 88
 |||||||
 QY 423 ctgtgcatagaanaaagaagtttgttaatttatattacttttagttgataactagt 482
 |||||||
 Db 87 CTGTGCATGAAAAAAGAGTTTGTATTTATTTACTTTTGTAGTTGATCTAAGT 28
 |||||||
 QY 483 attaacatatcttctgtattctcca 508
 |||||||
 Db 27 ATTAACATATTCTGTATTCTTCCA 2
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Search completed: July 17, 2002, 09:19:58
 Job time: 11688 sec

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From: 1 to: 37948

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      :|||||:::
6526 TATAACAGTTTGATA...CTAATAGTATTtttccctccta||

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45 IaleuileProgluThrThrLeu.....ThrVal 55

6570 CTATGCAGAAAGCTACGAATCCCTTCATCAGTAATAAGTAGTAATAACGGTT 6619

6620 ATGATTCGGCAGATGCGTATC.....TCAGTATGGTGTATGCGGAA.. 6661

12 IYRALEUUIEYIARGLYSLEULEUPHEASNPROSER.....GLYPROT 87
66662 ::::: :::::

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87 yrgln 88

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6690 ATCAG 6694

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name: /cgn2_6/ptodata/2/lna/6B-COMB.seq:US-09-116-498-11

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documentation_block: US/09116498
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GENERAL INFORMATION:

10

100

APPLICANT: Littman, Dan R.
 Deng, Hongkui
 Nuttman, Derya
 Ramani, Vineet N.K.
 TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
 ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
 IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
 THEREOF
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/116,498
 FILING DATE: 16-Jul-1998
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1083 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Pitali macaque
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-09-116-498-11

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Percent Similarity:	40.21		

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alignment_block:
    NC_009867.1

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.....GCAGAGAAAAAGG

567 TCCACTTAACTCATATGGTCCCTGGTGGCCTTAATTTTCACCTTTT

41 a l s e r v a l l e u a l a l e u l e p r o g l u t h r t h r t h r l e u t h r v a l g l y
|| ::::|||

01/ ICCCTTGTG.....

628AGCATTTGTGACCTCCTCCATCTTCTTTCTTT
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1

Thu Jul 18 17:22:02 2002

us-09-801-115-2.rni

Page 3

74 uiletyrArglystLeuPheasnProSerGlyProTyrGlnLysLysp 91
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658AGGAAGCTGTGTCATCCAT.....TACCAGCAATCAG 688
91 rovalHisGlnLysLys 96
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seq_documentation_block:

Sequence 7, Application US/09116498
Patent No. 6251582
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-116-498-7

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Ratio: 1.651 Gaps: 4
Percent Similarity: 48.315 Percent Identity: 26.966

alignment_block:
US-09-801-115-2 x US-09-116-498-7 ..

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567 TCACATTAACCTATGATGCTGCGTGCCTTAATTTACCTTTTGG 616
41 alSerValLeuAlaLeuIleProGlnThrThrLeuThrValGlyGly 57
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617 TCCCTTTGTTG..... 627
58 GlyValPheAlaLeuValThrAlaValCysCysLeuAlaSpGlyAlaLe 74
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628AGCATGTGACCTGCTACTGTTGCATTCGA..... 657
74 uiletyrArglystLeuPheasnProSerGlyProTyrGlnLysLysp 91
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seq_documentation_block:
Sequence 2, Application US/08061092A
Patent No. 5587458
GENERAL INFORMATION:
APPLICANT: KING, C R
APPlicant: KASPRZYK, Philip G
TITLE OF INVENTION: ANTI-erbB-2 ANTIBODIES, COMBINATIONS
THEREOF, AND THERAPEUTIC AND DIAGNOSTIC USES THEREOF

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22131-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,092A
FILING DATE: 14-May-1993
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 018797-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

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NAME/KEY: CDS
LOCATION: 1..720
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44 u.....AlaLeuIleProGluThrThrLeuThrValGly.... 56
   :::::::::::::::::::::
634 AGACGGCAGTGTCTCTCAGATGTCAGCTGCTGAGCTGAGTGAAGGCGCCG 585
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57 ..GlyGlyValAlaPheAlaLeuValThrAlaValCysCysLeuAlaAspGly 72
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584 TTGGAGGA.....TGTGTCTGCTGTATTAAGTGGCTT 553
   :::::::::::::::::::::
73 AlaLeuIleThrArgLys.....LeuLeuPheAsnPr 83
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552 GCCCTGGAATTGCGGTCAATATACAGTATTAACCATTCAGATGATGATCC 503
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seq_documentation_block:
; Sequence 12, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Boriack-Sjodin, Ann
; APPLICANT: Margalit, S. M.
; APPLICANT: Bor-Sogal, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228R
; CURRENT APPLICATION NUMBER: US/09/356,952
; EARLIER FILING DATE: 1999-07-19
; APPLICATION NUMBER: 60/093,631
; FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 43676
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-09-356-952-12

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; Patent No. 5759541
; GENERAL INFORMATION:
; APPLICANT: Bach, Alfred
; APPLICANT: Hillen, Heinz
; APPLICANT: Bialojan, Siegfried
; TITLE OF INVENTION: No. 5759541el Proteins, the Preparation and Use
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Keil & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
; COMPUTER: IBM AT-compatible, 80286 processor
; OPERATING SYSTEM: MS-DOS version 5.0
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,862
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,705
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,040
; FILING DATE: 30-DEC-1992
; APPLICATION NUMBER: PCT/EP91/01361
; FILING DATE: 19-JUL-1991
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Agkistrodon rhodostoma
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; LOCATION: 231 to 935
; OTHER INFORMATION: the coding region shown in (2)(ix)(b)
; US-08-684-862-9

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us-09-801-115-2.rml

Page 5

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39 leu1valserValleuAlaLeu1leProGluThrThrLeuThrVa 55
1295 CTTTATTATTCCTTCTTCCTCGATGCTGACATTTCTACAGTCATTT 1246
1245 TATCCAACTCTGTTCTTCTGCTCCGATTTAGTTGCTTACAGGAT 1197
72 lYAlaLeu1leuYrArgLysLeuLeuPheAsnProSerGlyProTyrGln 88
1196 .....AAGTTGTTTTCCTCAATCTCTGATTTTC... 1167
89 LysLysProValHisGlu 94
1166 .....CCCCCCCACAG 1155

seq_name: /cgn2-6/ptodata/2/lna/6B_COMB.seq:US-09-462-844-1

seq_documentation_block:
; Sequence 1, Application US/09462844
; Patent No. 6258563
; GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: Increasing Production of Proteins in
; FILE REFERENCE: GC385-US
; CURRENT APPLICATION NUMBER: US/09/462,844
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EP 97305286.3
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 97305344.0
; PRIOR FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Bacillus subtilis
; US-09-462-844-1

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Percent Similarity: 50.549 Percent Identity: 28.571

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US-09-801-115-2 x US-09-462-844-1 ..
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32 uValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProG 49
1182 TATCCACCTCCGCTTTC...TTATCGAGATTTCTCTGCTGCTCTGTGG 1228
49 lufThrThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProG 65
1229 AAGAGATGCTGTGATCGGAAAAAGGCTGTTGCT... 1266
66 ValCysCysLeuAlaAspGlyAlaLeuIleYrArgLysLeuLeuPheAs 82
1267 .....GTCAATTAAGAAACATATCATGCA 1289
82 n.....ProSerGlyProTyrGlnLys 90
1290 TATTGAGATACGATGAATAATACAGAGCCGATACGCCATTCACAAAT 1339
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seq_documentation_block:
; Sequence 14, Application US/08772270A
; Patent No. 6019984
; GENERAL INFORMATION:
; APPLICANT: MacInnes, Janet
; APPLICANT: Ricciatelli, Paul
; APPLICANT: Mallard, Bonnie
; APPLICANT: Rosendal, Soren
; TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
; TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Bereskin & Part
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3J2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,270A
; FILING DATE: December 23, 1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravalle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 6580-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Actinobacillus pleuropneumoniae
; US-08-772-270A-14

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Ratio: 1.240 Gaps: 4
Percent Similarity: 51.485 Percent Identity: 22.772

alignment_block:
US-08-801-115-2 x US-08-772-270A-14/rev ..
Align seg 1/1 to reverse of: US-08-772-270A-14 from: 1 to: 7721
22 LysMetLeuArgLeuAspLeuIleAsnSer..... 31
7519 CCTCTCTAGACCTTCAGTAATGATTCCTTAATGACTGATAGAA 7470
32 leuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleP 48
7469 ACTGATACACGCTGCTCTCTGTTTAATTCGCAATACGCTCATTC 7420
48 rogluThrThr.....ThrleuThrValGlyGlyValPheAlaLeu 62
7419 CAGAACCTAATGATTAATTCCTTATACCACTGTTAATGTTTCTGTTA 7370
```

63

ValThrAlaVal.....CysCysLeuAl 70

7369 ATCTCAATATAGAAATGAAACCAAGCTGAGGCTGCTCAATAGC 7320

70 AAspOlyAlaLeuIleTyrArg..... 77

7319 ATCAAGAGTAAATAGTACTTTTCCATAGAGATAACCATATCTGTGT 7270

78LysLeuLeuPheAsnProSerGlyProTyrGlnLys 90

7269 AGGAAAGTTTCCACTTAAATACCTGCTTCATTCATTTCAACAAA 7220

91 Pro 91

7219 CCA 7217

seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-08-976-259-70

```

seq_documentation_block:
; Sequence 70, Application US/08976259
; Patent No. 6316609
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Choi, G.H.
; APPLICANT: Welch, Rodney A.
; TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
; Patent No. 6316609
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,259
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488, 0740002/EKS/CBM
; TELEPHONE: (202) 371-2540
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17710 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-976-259-70

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US-08-976-259-70

alignment_scores:

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Quality: 64.00 Length: 100
Ratio: 1.231 Gaps: 3
Percent Similarity: 52.000 Percent Identity: 25.000

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US-09-801-115-2 x US-08-976-259-70

Align seg 1/1 to: US-08-976-259-70 from: 1 to: 17710

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US-09-801-115-2 x US-08-976-259-70
Align seg 1/1 to: US-08-976-259-70 from: 1 to: 17710

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ORIGINAL SOURCE:
ORGANISM: PAG1069RP
US-08-998-416-176

alignment_scores:
Quality: 63.50 Length: 109
Ratio: 1.351 Gaps: 5
Percent Similarity: 43.119 Percent Identity: 25.688

alignment_block:
US-09-801-115-2 x US-08-998-416-176 ..

Align seg 1/1 to: US-08-998-416-176 from: 1 to: 654

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28 1lelleasnerleuvalThrThrValPheMetLeuIleValSerValle 44
   ::::: :::::|||||::: ||::: ||| :::: |||
127 CTCGTGCTGCGCATGTCACGTCTACGAGCTGCGCCTCTCTGTCG 176
   44 uAlaLeuIle.....ProGIuThrThrLeuThrValGIyGIy.... 57
   ||| :::: |||:::|||||::: |||::: |||:::
177 TGTGCTGTGGGTATGCCGACGCGCGCCTCACACGCGCGCGCAC 226
   58 ..GIyAlPheAlaLeuValThr.....AlaValCysCysLeuAlaasp 71
   |||:::||||| |||::: |||::: |||::: |||:::
227 TTGGGCGCTTTCACATGCTCCAGCGTGAGCGCTGTGATGCTGTG 276
   72 .....GlyAlaLeuIleTyr..... 76
277 CTCCTCTCCGCCATTAAGTGGGAGCTGTATCTATGCTACTCAAGCT 326
   76 ..... 76
327 CGCGGTATAGCTTGTATATATATCTTACGCTGCGAGCGCCTATCCGA 376
   77 .....ArgLysLeuLeuPheAsnProSer 84
377 CACAGCTATATATTGGCCGCGCTCTCGCGCTGCTGGGAGCGCAT 426
   85 GIyProTyrGIuLysLysProValHis 93
   |||:::||||| |||::: |||::: |||:::
427 GACCCACACCTGATGTCGCTTGAC 453

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seq_name: /cgn2_6/plodata/2/lna/5B_COMB.seq:US-09-377-155-8

seq_documentation_block:

```

; Sequence 8, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1782)
; US-09-377-155-8

```

alignment_scores:

Quality: 63.50 Length: 77
Ratio: 1.512 Gaps: 3
Percent Similarity: 54.545 Percent Identity: 36.364

alignment_block:

US-09-801-115-2 x US-09-377-155-8/rev ..

Align seg 1/1 to reverse of: US-09-377-155-8 from: 1 to: 1785

```

11 ArgProPheCysPheSerValLysGIyHisValLysMetLeuArgLeuAs 27
   ::::: |||::: |||::: |||::: |||:::
926 AAGCCTTGCGCTTGTCTGTAGAAATCATCTCGCTTGTCTTAC 877
   27 pIleIleAsn.....SerLeuValThrThrValPheMet...L 39
   ::::: |||::: |||::: |||::: |||:::
876 AGTACCAACTTACCGCTTTTCTTGTATACAGAAAGTCTTCGACCGA 827
   39 euIleValSerValLeuAlaLeuIleProGIuThrThrLeuThrVal 55
   ::::: |||::: |||::: |||::: |||:::
826 TTTAACCTTGCGTCTCTTGGCGTGTCTTGTTCACATTAACAGTC 777
   56 GIyGIyAlaValPheAlaLeuValThrAlaValCysCysLeuAlaasp 72
   |||::: |||::: |||::: |||::: |||:::
776 GTTGTCTTGTATCTGCGCTCAAGACATCGACTGTGTGAATGTCGAC 727
   72 LyAlaLeuIleTyrArgLysLeuPhe 81
   |||::: |||::: |||::: |||::: |||:::
726 GAAATCAACGTTATCGGAAGCTGTGTAC 698

```

seq_name: /cgn2_6/plodata/2/lna/5B_COMB.seq:US-09-669-974-8

seq_documentation_block:

```

; Sequence 8, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1782)
; US-09-669-974-8

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alignment_scores:
Quality: 63.50 Length: 77
Ratio: 1.512 Gaps: 3
Percent Similarity: 54.545 Percent Identity: 36.364

alignment_block:

US-09-801-115-2 x US-09-669-974-8/rev ..

Align seg 1/1 to reverse of: US-09-669-974-8 from: 1 to: 1785

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11 ArgProPheCysPheSerValLysGIyHisValLysMetLeuArgLeuAs 27
   ::::: |||::: |||::: |||::: |||:::
926 AAGCCTTGCGCTTGTCTGTAGAAATCATCTCGCTTGTGTTCAC 877

```

```

27 pileleasn.....SerleuValThrThrValPheMet...L 39
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
876 AGTACACCACTTACCGCTCTTTTCTTGATACAGAGCTTTCGCCACCGA 827
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
39 euileValSerValleuAlaValleuProGluThrThrThrVal 55
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
826 TTTTAACCTGCGTCTCTGCGCTTCTTGGCTTCCACATTAACAGTCT 777
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
56 GlyGlyGlyValPheAlaValThrAlaValCysCysLeuAlaAspG 72
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
776 GTTGTCTTTCGATCTGCGCTCAAGACTGCTGCTGTAAGTCGCGAC 727
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
72 LyaAlaLeuIleTyrArgLysLeuPhe 81
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
726 GAATCAACGTTATCGAAGCTGTTCTTAC 698

seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-09-367-206-6

seq_documentation_block:
: Sequence 6, Application US/09367206
: Patent No. 6326482
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: TITLE OF INVENTION: NSP Molecules
: FILE REFERENCE: P1223RIE
: CURRENT APPLICATION NUMBER: US/09/367,206
: CURRENT FILING DATE: 1999-08-09
: PRIOR APPLICATION NUMBER: PCT/US99/08847
: PRIOR FILING DATE: 1999-04-23
: PRIOR APPLICATION NUMBER: US 60/082,767
: PRIOR FILING DATE: 1998-04-23
: PRIOR APPLICATION NUMBER: US 60/113,296
: PRIOR FILING DATE: 1998-12-22
: NUMBER OF SEQ ID NOS: 35
: SEQ ID NO 6
: LENGTH: 2153
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-367-206-6

alignment_scores:
Quality: 63.50 Length: 112
Ratio: 1.095 Gaps: 5
Percent Similarity: 51.786 Percent Identity: 24.107

alignment_block:
US-09-801-115-2 x US-09-367-206-6 ..

Align seg 1/1 to: US-09-367-206-6 from: 1 to: 2153

20 HISVALYSMetLeuArgLeuAspIleIleAsnSerleuValThrThrVa 36
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1452 CATGGCCGCGACCTAGCTAGACCTGCTGAAAGTTCCACACCATGTC 1501
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
36 LpMetLeuIleValSerValleu..... 44
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1502 CATCATGCTGCGCGTGCATCTCTGGGCTCACCGGCTGCGGAGAGC 1551
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
45 .....AlaLeuIleProGluThrThrThrLeuThrValGly..... 56
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1552 GGGAGCGCTGCTGCACAGACCATTCAGCTGGGCGCGAGCTACGGGG 1601
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
57 .....GlyGlyValPheAlaValThrAlaValCysCysLeu..... 69
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1602 ACTATGGCACAACATGTTCACTTCGCGCGTCAATGGTGCCTGACAT 1651
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
69 ..... 69
1652 GGCTGAGATTTCGGCTGGAGAGACATGGGTGACCTCGGCGAGCGAC 1701
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
70 ..AlaAspIleAlaLeuIleTyrArgLysLeuPheAsnProSerGly 85

```

```

1702 ACACAGAGGGTGCATCTCTGACGAGAAAGAGCTC.....AAG 1739
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
86 ProTyrGlnLysLysProValHISGlnLysLysGlu 97
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1740 CCTTTTCTCAAGAGC...CTCAAGAGGCGCAAGAA 1772
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-249-420-1

seq_documentation_block:
: Sequence 1, Application US/08249420
: Patent No. 5484724
: GENERAL INFORMATION:
: APPLICANT: El-Sherbeini, Mohamed
: APPLICANT: Clemas, Joseph
: TITLE OF INVENTION: DNA ENCODING GLS1
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Christine E. Carly
: STREET: 126 E. Lincoln Avenue
: CITY: Rahway
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07065-0900
: COMPUTER READABLE FORM:
: MEDIUM TYPE: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/249,420
: FILING DATE: 26-MAY-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Carly, Christine E.
: REGISTRATION NUMBER: 36,099
: REFERENCE/DOCKET NUMBER: 19162
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 594-6734
: TELEFAX: (908) 594-4720
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1854 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
US-08-249-420-1

alignment_scores:
Quality: 63.00 Length: 27
Ratio: 3.150 Gaps: 0
Percent Similarity: 74.074 Percent Identity: 51.852

alignment_block:
US-09-801-115-2 x US-08-249-420-1 ..

Align seg 1/1 to: US-08-249-420-1 from: 1 to: 1854

8 IleySHsArpProPheCysPheSerValLysGlyHISValLysMetLe 24
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
544 ATTATCCACAAGCAATTTTGTAACAAGTGAAGGTTGAACTAATATCT 593
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
24 AATGLeuAspIleIleAsnSerleuValThr 34
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
594 TCGCTAGAACCAATGAAATTCATCTGTTACT 624

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 17, 2002, 06:04:05 ; Search time 1777.03 Seconds
(without alignments)
4055.854 Million cell updates/sec

Title: US-09-801-115-1
Perfect score: 534
Sequence: 1 gtcccaactcgaagtgaag.....aaaaaaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estcl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505.8	94.7	524	10	BG705303 602687808
2	492.4	92.2	962	10	BG249994 602362062
3	491.8	92.1	510	10	BF399486 UI-R-CA1-
4	487	91.2	781	10	BG529072
5	485.4	90.9	487	10	BM472086
6	482.4	90.3	534	10	BG031757
7	468.2	87.7	529	10	BF691818 602247787
8	468	87.6	468	10	BF109912 7171f03.x
9	467.6	87.6	930	10	BF203359 601865968
10	462	84.6	452	9	AT078580 0237005.x
11	445	83.3	453	9	AT1743235 w990402.x
12	432.4	81.0	533	9	AV754613
13	430.4	80.6	432	9	AA429945 2w67f10.s
14	427	79.0	427	9	AA455042 aa04a07.s
15	422	77.8	423	9	AT128804 9a94d08.s
16	415.2	77.5	443	10	BG613984 602641513
17	413.8	77.5	432	9	AV759888 602641513

18	412.4	77.2	543	10	BG532587
19	403	75.5	815	10	BF215121
20	402.6	75.4	409	9	AT826623 wk35d10.x
21	399.4	74.8	402	9	AT989747 wu21f09.x
22	399	74.7	399	9	AA516431 ne58a03.s
23	394.4	73.9	396	9	AM183193 xj67f11.x
24	391	73.2	391	9	AT1989739 wu21e10.s
25	386	72.3	386	9	AA911088 ok67e01.s
26	384.4	72.0	386	9	AA989129 or75h10.s
27	381	71.3	395	9	AT141284
28	374.4	70.1	468	10	W52820
29	363	68.0	522	10	W38899
30	361.6	67.7	389	9	AA305052
31	357.6	67.0	456	10	BE875161
32	353	66.1	353	9	AT265924
33	349.4	65.4	692	11	AF151058
34	337.6	63.2	409	10	N89912
35	337.2	63.1	380	9	AA477156
36	331.4	62.1	333	9	AA987264
37	329.8	61.8	789	10	BE737159
38	327.6	61.3	381	9	AA644621
39	326.2	61.1	331	10	BF388158
40	324.4	60.7	326	9	AT263261
41	324	60.7	325	9	AT371387
42	319.4	59.8	678	10	BI561562
43	319	59.7	319	9	AT349474
44	317.6	59.5	491	10	W19506
45	306	57.3	332	10	BG940590

ALIGNMENTS

RESULT 1
LOCUS BG705303 524 bp mRNA linear EST 07-MAY-2001
DEFINITION 602687808F1 NIH-MGC_95 Homo sapiens CDNA clone IMAGE:4820568 5',
mRNA sequence.
ACCESSION BG705303 GI:13979504
VERSION BG705303.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 524)
AUTHORS NIH-MGC
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL Unpublished (1999)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: L1AM10725 row: 0 column: 01
High quality sequence stop: 521.
Location/Qualifiers
1..524
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4820568"
/clone_id="NIH-MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI; xhoI (ctgacg
); Oligo-dT primed using primer 5'-TTTATTTTATTTTATTT-3',
size-selected for average insert size 2.5 kb and

FEATURES

source

normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carinci, in preparation). Library constructed by M. Brownstein (NIH/NCBI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 142 a 113 c 138 g 131 t
ORIGIN

Query Match 94.7%; Score 505.8; DB 10; Length 524;
Best Local Similarity 99.6%; Pred. No. 4.6e-62;
Matches 507; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 gtgaagccagagctggtgaggaagtaggagggcggtgctccgcgcggtggtgct 74
D 4 GGGAGGCGGAGCTGGGAGAGTAGTAGGGAGGGCGGTCTCCGCGCGGTGCT 63
QY 75 atgccttcagagaacctaactagcagcagcagcagcagcagcagcagcagcagc 134
D 64 ATGCTTCGCGAGAACTTACCTCAGCAGCAGCTGAGAAAGATTGAGGAAAGTGCCTG 123
QY 135 ctgggtctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 194
D 124 CTGGGTCTGACAGACGATGATATACGCGACCGCAAAATTAACATGCGCCCTTCTGCT 183
QY 195 tcaagtgtgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 254
D 184 TCAGTGTGAAGGCGACAGTGAAGATGCTGCGGTGATATTATCACTCAGTGTGAACAA 243
QY 255 cagatattcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 314
D 244 CAGTATTACGCTCATCTGATCTGTGTGTCAGTATCAGAAACCAACATTTGACAG 303
QY 315 ttgggtgaggggt 374
D 304 TTGGTGGAGGGGTTGT 363
QY 375 tttaacggaagctctgttcaatcccgagcgtcttaacggaagcgtgtgtgtgtgt 434
D 364 TTTTACCGGAGGCTGT 423
QY 435 aaaaagaagcttctgttaatttatttatttatttatttatttatttatttatttattt 494
D 424 AAAAAAGAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 483
QY 495 tctgtatttcccaaaaaaaaaaaaaa 523
D 484 TCTGTATTCTTCCAAAAA 512

RESULT 2
BG249994 962 bp mRNA 1linear EST 13-FEB-2001
LOCUS 602362062P1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4470662 5',
DEFINITION mRNA sequence.
ACCESSION BG249994
VERSION BG249994.1 GI:12759810
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 962)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs@email.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10288 row: k column: 15
High quality sequence stop: 516.
Location/Qualifiers

FEATURES
source

1..962
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4470662"
/clone_id="NIH_MGC_90"
/issue_type="adenocarcinoma, cell_line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Liver; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; Oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC Library."
BASE COUNT 334 a 199 c 288 g 141 t
ORIGIN

Query Match 92.2%; Score 492.4; DB 10; Length 962;
Best Local Similarity 99.6%; Pred. No. 2.5e-60;
Matches 504; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 29 ggggagaagtagggagggcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 88
D 1 GCGGAGAGTAGGGAGGGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
QY 89 cctactcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 148
D 61 CCTACTCAGGACAGCCAGCTGAGAGAGTTGAGGAAAGTCTGCTGTGTGTGTGTGTGTGT 120
QY 149 gcgatgatacgtgtgacgcggaataaataacatcgccttctgtctcaagtgtgaaagc 208
D 121 GCGATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 209 caggtgaagatgt 268
D 181 CACGTGAAATGCTGT 240
QY 269 atcgtatctgt 328
D 241 ATCGTATCTGT 300
QY 329 ttgtgactgtgtgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 388
D 301 TTTGCACTTGTGACAGCAGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 389 ctgttcaatcccgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 448
D 361 CTGTCATATCCAGGCGGTCTTACAGAAAAAGCCGTGTGTGTGTGTGTGTGTGTGTGTGT 419
QY 449 taattttatttatttatttatttatttatttatttatttatttatttatttatttattt 508
D 420 TAAATTTTATTTACTTTTGT 479
QY 509 aaaaaaaaaaaaaaaaaaaaaa 534
D 480 CAAAAA 505

RESULT 3
BF399486 510 bp mRNA 1linear EST 27-NOV-2000
LOCUS BF399486/c
DEFINITION UT-R-CAL-bjb-b-12-0-UI.s1 UT-R-CAL Rattus norvegicus cDNA clone
UT-R-CAL-bjb-b-12-0-UI 3', mRNA sequence.
ACCESSION BF399486
VERSION BF399486.1 GI:11384494
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 510)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-Yes.

FEATURES
Source Location/Qualifiers
1..510
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CAL-bjb-b-12-0-UI"
/clone_1db="UI-R-CAL"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pMT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAL
library is a subtracted library derived from the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
and hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratseq.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_SEQ=None found"

BASE COUNT 130 a 131 c 104 g 145 t
ORIGIN

Query Match 92.1%; Score 491.8; DB 10; Length 510;
Best Local Similarity 99.6%; Pred. No. 4,3e-60;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

28 gggcggaagtagggagggaggtgctgcgcgcgcgtggtgctatcgctcgaga 87
|||||
495 GGGCGGAAGTAGGGAGGGGCGGTGCTCCGCCGCGGTGCTATCGCTCCGAGA 436
|||||
88 acctactcagcagcagctgagaagagtgaagaaagtctgctgctgctgcaga 147
|||||
435 ACCTACTCAGCGCAGCTGAGAGAGAGTGAAGGAAAGTCTGCTGCTGCAGCA 376
|||||
148 cgcgcatgataagtcgagcgcgaataaacaatgcgcctctgcttcagttgaag 207
|||||
375 CGCGATGGAATACGTGACGCCGAATAAATCAATGCCCTTCTGCTTCAGTGAAG 316
|||||
208 ccaacgtaagaatctgctgctgataatatacaactcactgttaacaacagtatcatgct 267
|||||
315 CCACGTAATGATCTGCGGTGATATTAATCACTCACTGTAACAACAGATTCATGCT 256
|||||
268 catcgatctgtgttgcactgataccagaacacacaacatgcaattgttgagaggt 327
|||||
255 CATCGATCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 196
|||||
328 gtttgcactgttgacagcagatgctctctgcagacgggagcccttattacggaaagt 387
|||||
195 GTTTCACCTTGTGACAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 136

QY 388 tctgttcaatcccaagggtgcttctaccagaaaagccctgtgcatgaataaaagaagttt 447
|||||
DB 135 TCTGTTCAATCCACAGCGGTCTTACCAAGAAACCGCTGATGATAAAAAAGAGTTT 76
|||||
QY 448 gtaattataattacttttagtttgatgactaagatalttaacatattctgtatcttc 507
|||||
DB 75 GTAATTTATATTAATCTTTTGTGTTGATTAAGTAATTAACATATTTGTTATCTTAA 16
|||||
QY 508 aaaaaaataaaaaa 522
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 4
BG529072 781 bp mRNA linear EST 03-APR-2001
LOCUS 602579169P1 NIH_MGC_60 Homo sapiens CDNA clone IMAGE:4713305 5',
DEFINITION mRNA sequence.
ACCESSION BG529072
VERSION BG529072.1 GI:13520609
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 781)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DPV
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
<http://image.llnl.gov>
Plate: L10C1556 row: 1 column: 18
High quality sequence stop: 475.

FEATURES
Source Location/Qualifiers
1..781
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1db="NIH_MGC_60"
/clone_1db="IMGE:4713305"
/tissue_type="adrenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggcattggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAAGGCGGAGGCGGCGACATG-dT(30)BN-3
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts and was constructed by Clontech
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

BASE COUNT 228 a 157 c 233 g 163 t
ORIGIN

Query Match 91.2%; Score 487; DB 10; Length 781;
Best Local Similarity 98.7%; Pred. No. 1.6e-59;
Matches 512; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 17 gaacccagagctggcgaagaagtagggagggcgtgtctcgcgcgcgtggtgctat 76
|||||
DB 1 GAAGCGAGCTGGGCGAAGATAGGAGGCGGTGCTCCGCCGCGGTGCTAT 60
|||||
QY 77 cgttcgagaagacttaccagcagcagctgagaagagttgagggaagtgctgct 136

Db 61 CGCTTGCAGAAACCTACTCAGCGAGCCAGCTGAGAAAGATTGAGGGAAAGTGTCT 120

Qy 137 gggcttcgcagacgcgatgataaactgacgtgcagccgaaaaaaataaacatgcgcccttcgttc 196

Db 121 GGGCTTCGACAGACCCGATGATACGTCACCGCAAAATAAACATCGCCCTTCGTTC 180

Qy 197 agtgtaaaggccacgttgaagatgctgcggcctgataataatcaactcactgtgaacaca 256

Db 181 AGTGTAAAGGCCACTGAAAGATGCTGCGCGCTGGATATTATCACTCACCTGATAACACA 240

Qy 257 gtaattcatgcatactcgtactcgtgtgtggacatgataccgaaaccacaaattgaacgt 316

Db 241 GATTCAATGCTATCGTATCTGTGTGGCACTGATACCGAAGAAACCAACATTGACAGTT 300

Qy 317 ggtggaagggtgtttgcaacttgtgaacagatagctgtctgcgaaggggccctatt 376

Db 301 GGTGAGGGGTTGTTCACCTTGTAACAGAGATGCTGTCTTGCCACAGGGGCTTTATT 360

Qy 377 taccggaagctctgttcaatccacagcggctcctaccagaaaaagcctgtgcaaaaaa 436

Db 361 TACCGGAAGCTTCTTTCAATCCACGCGGCTCTTACCAAGAAAAAGCGCTTGCAATGAAAA 420

Qy 437 aagaagaatttgtaatttatatactctttagttagttaaactaagbataaacataatc 496

Db 421 AAAGAG-TTTGTAATTTTATATATTCCTTTTAACTTGTACTAAAGTATTAAACATATTTC 479

Qy 497 t-gtattcttccaaaaaaataaaaaaaataaaaaa 534

Db 480 TGTGATTCTTCCAGAAAGAGAAAAAAGAAAAAGAAAGAAAA 518

RESULT	5
LOCUS	BM472086
DEFINITION	BM472086 487 bp mRNA linear EST 05-FEB-2002
ACCESSION	AGENCECOURT_6469731 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:5576339
VERSION	5'', mRNA sequence.
KEYWORDS	BM472086 BM472086.1 GI:18521128
SOURCE	EST.
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 487) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rcgabs+email.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) Clone distribution by: Agencourt Bioscience Corporation found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov plate: LLM12328 row: a column: 12 High quality sequence stop: 486. location/Qualifiers 1..487

BASE COUNT

ORIGIN

Query Match	90.9%	Score 485.4;	DB 10;	Length 487;
Best Local Similarity	99.8%;	Pred. No. 3.4e-59;		
Matches 486;	Conservative	0;	Mismatches 1;	Indels 0;

[illegible]

```

RESULT      6
LOCUS       BG031757
DEFINITION  BG031757
ACCESSION   BG031757
VERSION     BG031757
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 534)
            NIH-MGC http://mgc.nci.nih.gov/,
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DRP
            CDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LRAM10089. row: e column: 06
            High quality sequence stop: 446.
            Location/Qualifiers
                1..534

```

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4394093"
 /clone_lib="NIH_MGC-87"
 /tissue_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: breast; Vector: PCMV-SPORE6; Site:1; NotI;
 Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 163 a 108 c 132 g 131 t
 ORIGIN

Query Match 90.3%; Score 482.4; DB 10; Length 534;
 Best Local Similarity 98.2%; Pred. No. 8.6e-59;
 Matches 499; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 30 gcgagaagtagggagggcggtgctccgcccgggtggtgctatcgtccgcgaac 89
 DB 1 GCGAGAAGTAGGGAGGGGGGTGCTCCCGCGGGTGGGCTATCGCTTCGCGAAG 60
 QY 90 ctactcagccagccagcgtgagaagagttgagggaaagtgtgtgtgtgtgtgtgtgt 149
 DB 61 CTACTCAGCCAGCCAGCAGTGAAGAGTGAAGGAAAGTGTGTGTGTGTGTGTGTGT 120
 QY 150 cgaatgataacgtgcaagcgaataaataacatccctcctcgtcagttgtgaaagcc 209
 DB 121 CGATGATGAACGTGCGACCGGAAATGAATGAATGAATGAATGAATGAATGAATGA 180
 QY 210 acggaagaatctgctggtgtgatatatcaactcactggttaacaacagatcatcga 269
 DB 181 ACGGAAGATCTGGGCTGGATTTATCACTCACTGTAACACAGATTTATCTCTCA 240
 QY 270 tcgtaatcgtgtgtgacatgtatatacagaacaacacatgtggtgtgtgtgtgtgt 329
 DB 241 TCGTATCTGTGTGTGCTGCTGATACCAAGAACCAATTTGAGTGGAGGGGTGT 300
 QY 330 ttgcaactgtgacagcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 389
 DB 301 TTGCACTTGTGACACAGATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
 QY 390 tgttaacatcccggt 449
 DB 361 TGTTAATCTCCAGCGGCTCTTACAGAAAAAGCTGTGTGTGTGTGTGTGTGTGTGT 420
 QY 450 aatttataatcttcttgaattgtatctaaag--tattaaacataatctgtatcttc 506
 DB 421 AATTTATATTAATCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 QY 507 caaaaaaataaaaaaataaaaaa 534
 DB 481 CCCACAAAAAATAAAAAAATAAAAAA 508

RESULT 7
 BE691818 529 bp mRNA linear EST 22-DEC-2000
 LOCUS 602247787.1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333244 5',
 DEFINITION mRNA sequence.
 ACCESSION BE691818
 VERSION BE691818.1 GI:11977226
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 529)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCID/DPN
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM1200 row: m column: 21
 High quality sequence stop: 483.

FEATURES
 source
 1..529
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4333244"
 /clone_lib="NIH_MGC_62"
 /tissue_type="melanotic melanoma, high MDR"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pMDR-LIB (Clontech); Site:1:
 SfiI (99ccatctggcc); Site:2: SfiI (99ccatctggcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-ATTCTAGAGGCCGAGCGGCCGACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

BASE COUNT 139 a 119 c 138 g 133 t
 ORIGIN

Query Match 87.7%; Score 468.2; DB 10; Length 529;
 Best Local Similarity 98.2%; Pred. No. 8.4e-57;
 Matches 484; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 23 gactgagcgaagtagggagggcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 82
 DB 2 GAGCTGGGGCTAGAGTAGGCGGAGGGGCTGCTCCCGCGGGTGTGTGTGTGTGTGTGT 61
 QY 83 gcgaactactcagcagccagcgtgagaagagttgagggaaagtgtgtgtgtgtgtgt 142
 DB 62 GCAGAACCTACTCAGGACGCGCTGAGAGAGTTGAGGAGAGTGTGTGTGTGTGTGTGT 121
 QY 143 gcagacgcatgataacgt 202
 DB 122 GCAGACGGGATGATACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 181
 QY 203 aaagccacgtgaaagt 262
 DB 182 AAAGCCACGTAAGATGCTGCGGCTGATATATCACTCACTGTATCAACAGTATTC 241
 QY 263 atgtccatcgtatcgt 322
 DB 242 ATGCTCATCTGATTCGT 301
 QY 323 ggggt 382
 DB 302 GGGGT 361
 QY 383 aagcttctgtatcccgagcgt 441
 DB 362 AAGCTTGT 421
 QY 442 agtttgaatttatattacttttgaatttgaatttgaatttgaatttgaatttgaattt 501
 DB 422 AAGTTGTATTTTATATTACTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 481
 QY 502 tcttccaaaaa 514
 DB 482 TCTTGGGAAGAA 494

RESULT 8
 BFI09912/C
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 468)
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 This clone is available royalty-free through LINC; contact the
 IMAGE Consortium (infoimage.linc.nih.gov) for further information.
 Seq primer: -40UP from Gibco.
 Location/Qualifiers

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3526805"
/clone_1fb="Soares_NSF_F8_9W_OT_PA_P1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7n3-Pac (Pharmacia) with
a modified polylinker; site.1: Not I; site.2: Eco RI,
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NbHSF pool 1:
309384-310919, 333208-325895 Soares Nb2HP pool 1:
145032-147335, 147720-148103, 148872-149255 15002 -
150407, 151176-152337 Soares Nb2HR8-9W pool 1:
758280-760583 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NbHOT
pool 1: 723720-726407, 733080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

```

	Query Match	Best Local Similarity	87.6%: Score 468; DB 10;	Length 468;
	Matches	468; Conservative	0; Mismatches	0; Indels
			0; Gaps	0;
QY	46	ggcggtgtccgcgcgcggtggcggtgtgtatcgcgtccgaagaactactcaagcagcag	105	
Db	468	GGCGGTGCTCCGCCCGCGGTGGGGTGGTATCGCTCCGACAGAACTTACTCAGCGACCG	409	
QY	106	ctgagaagaagttggagggaaagtgcctgcctgcctgggtctcagaacgcagtgaatacgtga	165	
Db	408	CTGAAAGAGTTGAGAGGAAAGTGCCTGCTGGGCTCTCAGACGCGAAGGATTAACGTGCA	349	
QY	166	ggcgaaataaacaatcgccctcttgccttgaagtgtgaagggccacgtgaagaatgcttcg	225	
Db	348	GCCGAATAATAACAATGCCCCCTTCTGCTTAAAGTGTGAAGGCCACGGAAAGATGCTCG	289	
QY	226	gctcgtatattatcaactactcgtgtaaacaagratltaactgtcatcgtatcgtgtgtgc	285	
Db	288	GCTGGATTTTTCACACTCCTCGTAAACAACAGTATTCATGCTCATCGTATCTGTGGTGC	229	
QY	286	actataccagaaacccaacatctgacaggttgggtggaggggtgttggactctgtgaacgc	345	

Db	228	ACTGATATACAGAAACCAACAACTTGACAAATTGGTATGAGGGGTGTTGGCACTGTGTGACAC	169
QY	346	agtaatgcgtctcttgcgcacgagggccctattaccggaaagctctgttcaatccacgag	405
Db	168	ACTATGCTGTCCTTGGCGACGGGGCCCTTATTACCGAGACTTCGTGTAATCCAGGG	109
QY	406	tccctaccgagaaagccgtgcatcgtgaaaaaaagaagcttctgtaatttatactt	465
Db	108	TCCCTTACCGAGAAAGCCCTGTCAATGAAAAAAGAAAGTTGTATTTATTTATTTACTTT	49
QY	466	ttagtttgatactaaglattaaacaattctgtatctcttccaaaaa	513
Db	48	TTAGTTTGATACTAAGTATTTAACTATTTCTGTCTTCTTCCAAAAA	1

RESULT	9				
LOCUS	BF203359				
DEFINITION	BF203359	930 bp	mRNA	linear	EST 06-NOV-2000
ACCESSION	60186596881	NIH-MGC_17	Homo sapiens	CDNA clone	IMAGE:4098496 5',
VERSION	BF203359				
KEYWORDS	BF203359.1	GI:11096945			
SOURCE	EST.				
ORGANISM	human.				
REFERENCE	Human sapiens				
AUTHORS	Emmalyrola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
JOURNAL	1 (bases 1 to 930)				
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .				
	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, ph.D.				

```

FEATURES
SOURCE
    CNA Library Preparation: Ling Hong/Rubin Laboratory
    CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LNLN at: Image.lnl.gov
    Plate: ULM965 row: h column: 17
    High quality sequence stop: 537.
    Location/Qualifiers
        1..930
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:4038496"
        /clone_lib="NH-MGC-17"
        /tissue_type="rhaddomysarcoma"
        /lab_host="DH10B (phage-resistant)"
        /note="Organ: muscle; Vector: pORF7; Site_1: EcoRI;
        Site_2: XhoI; cDNA made by oligo-dT priming.
        Directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGCACGAC(G). Size-selected >500bp
        for average insert size 1.8kb. Library constructed by
        Ling Hong in the laboratory of Gerald M. Rubin (University
        of California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT
318 a 203 c 257 g 152 t
ORIGIN

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Query Match	87.6%	Score 467.6	DB 10	Length 930
Best Local Similarity	98.6%	Pred. No. 7.5e-57		
Matches 503	Conservative	0	Mismatches 4	Indels 3
QY	25	gctggcagagaaagtgggagcggtgctccgcgcggttgccgttcacgccttgc	84	
Db	1	gctggcgcacaaagtagggagagccgctctccgcgcgcggtgctatccgttcgc	60	
QY	85	agaacctactaacgacagcagctggaagaagtttggagaaagtgtgctgcgtgggtctgc	144	
Db	61	agaacctatctcagcagcagccactcagagaagattgtagggaaatcgtctcctgcctgggtctgc	120	

QY 145 agacgcgatgataacgtgcagccgaataataacatgcacctctctgcttcagtgtga 204
 DB 121 AGAGCGATGATGATACGCGACCGCAAAATATAACATGCCCCCTTCTGCTTACGTGTA 180
 QY 205 aggcacgtgaagatgctgcgcgtgatattatcaactcactgtgtaacacagattatc 264
 DB 181 AGGCGACGTGAAGATGCGCGCGGTGATATTATCAACTGACATGTAACACAGTATTAT 240
 QY 265 gctcatcgtatctgtgttgacgtatccagaacccaacattgacagtgtgtggaag 324
 DB 241 GCTCATGATCTGTGTGGCAGTGTACAGAAACCAACAACTTGACAGTTGGTGTGAAG 300
 QY 325 ggtgttgacattgtgacgaagatgctgtcttcgcagcgggcccattattaccgga 384
 DB 301 GGTG-TCGCACTTGACAGAGATGATGCTGCTTCCGACGGGGCCCTTATTACGGGA 359
 QY 385 gctcctgtcaatccacagcgttcctaccagaanaaagcctgtgtaaaaaaagaagt 444
 DB 360 GCTTCTGTCAATGCCACGGGCTTACAGAAAAAGCCTGTGATGAATAAAAAAGAG- 418
 QY 445 ttgttaattatattacttttagttgatactaagtaattacattctctgtattct 504
 DB 419 TTTGTAATTATTATATTACTTTTAA-TTGATACTAAGTATTAAACATTTTCTGTATCT 477
 QY 505 tccaaaaaataaaaaaataaaaaa 534
 DB 478 TCACAAAAAATAAAAAACAAAAA 507

RESULT 10 452 bp mRNA linear EST 10-AUG-1998
 A1078580/c
 LOCUS 0237h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1677561
 DEFINITION 3', mRNA sequence.
 ACCESSION A1078580
 VERSION A1078580.1 GI:3412988
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 452)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Journal
 COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40m13 fwd. ET from AmerSham
 High quality sequence stop: 410.
 Location/Qualifiers
 1..452
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1677561"
 /clone_lib="Soares_NHMPu_S1"
 /tissue_type="pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pT7T3D-Pac
 (Pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NDM, pregnant uterus
 NDHPV, and fetal heart NBH119W) were mixed, and as circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

BASE COUNT

125 a 110 c 97 g 120 t

ORIGIN

Query Match 84.6%; Score 452; DB 9; Length 452;
 Best Local Similarity 100.0%; Pred. No. 1.7e-54;
 Matches 452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 cgcggtgctgtgtatcgtcttcgcagaactactcagcagcagctggaagattg 118
 DB 452 CGCGGTGCGGTTGCTTTCGTTGCGAAGACCTACTGAGCGACGCTGAGAAAGTTG 393
 QY 119 agggaaagtgctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 178
 DB 392 AGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333
 QY 179 catgccccttctctcagtgatgaagagcagtgatgagctgtgtgtgtgtgtgtgt 238
 DB 332 CATGCCCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 273
 QY 239 aactcactgtgaacaacagatattcatgtcatcgtatctgtgtgtgtgtgtgtgtgt 298
 DB 272 AACTCAGTGTGATACAAAGTATTCATGCTCATGCTATGCTGTGTGTGTGTGTGTGT 213
 QY 299 accaacaattgacagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 358
 DB 212 ACCAACAATGTAACAGT 153
 QY 359 gccgagcggggcccttattaccggaagcttctgtcaatccagcagctcaccagaa 418
 DB 152 GCCGAGCGGGCCCTTATTATCCGGAAGCTTCGTTCATCCACGCGGTCTTACCGAANA 93
 QY 419 aagcctgtcatalgaanaaagaagttgttaattatattacttttagttgact 478
 DB 92 AAGCCTGTGCAATGAAAAAAGAGTTTGTATTATTATTACTTTTATTGTTGATCT 33
 QY 479 aagatttaacattattctgtattcttccaa 510
 DB 32 AAGTATTAAACATATTCTGTATCTTCANA 1

RESULT 11 453 bp mRNA linear EST 20-DEC-1999
 A1743235/c
 LOCUS wg90a02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 DEFINITION IMAGE:2372330 3', mRNA sequence.
 ACCESSION A1743235
 VERSION A1743235.1 GI:5111523
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 453)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Journal
 COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 378 Std Error: 0.00
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1..453
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2372330"
 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized

	ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
	REFERENCE	1 (bases 1 to 432)
	AUTHORS	Hillier,L., Allen,M., Bowles,D., Dubuque,T., Geisels,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Merri,M., Martin,J., Moore,B, Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie, ,T., Waterston,R. and Wilson.R. Washu-Merck EST Project 1997 Unpublished (1997)
	TITLE	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu
	JOURNAL	This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -4lnl3 fwd. Ef from Amersham High quality sequence stop: 421.
	COMMENT	Location/Qualifiers 1..432 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:781291" /clone_1id="Soares_testis_NHT" /sex="male" /lab_host="DH10B" /note="Vector: pUT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories , Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTCGAAGCGGGCCGCCCAATTGTGTTTTTTT 3'] (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pUT73 vector. Library went through one round of normalization to Cots, and was constructed by Bento Soares and M. Fatima Bonaldo."
	BASE COUNT	119 a 101 c 92 g 120 t
	ORIGIN	
	Query Match	80.6%; Score 430.4; DB 9; Length 432;
	Best Local Similarity	99.8%; Pred. No. 1.9e-51;
	Matches 431; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	81	tgcgaacctactcagcgccagctgtaagaagtgtgaaggaaatgctgctgagt 140
DB	432	TGCcAgAACtACTAcAGcAGcAGCcAGcAGTtGAGGAAAGTtcTcTcTGGcT 373
QY	141	ctgcagacggcatggataacgtgcagccgaataaacatcgccctctgcttcagt 200
DB	372	CtGcAGAcGcGgAtGgAATGcAGTcGAGCgGAAAAACAATcGcCCTTcGTTCAgTg 313
QY	201	tgaagaagccacgtygaagatcctgcggttgatatattacaactcaactcagttgaacaacagat 260
DB	312	TGAAGAAGCCAcGtGAAGATcTcGcGcTcGATATtATfAACtAcTcTcGTtAAcAcAGtAT 253
QY	261	tcatgtcatcgtatctgtgttgacctgatlaccagaacaacacaatalgacagttggtg 320
DB	252	TcATtGcTcATcAGTATcTGTtGtGcATcGTATtACCAGAAACcACAAcATtGACAGTtGtG 193
QY	321	gaagggttgtttgtagctgtgacagcagatacgtcgtcttgcgcagcgagccctatttac 380
DB	192	GAGGgGtTtGcAcTtTGAcAGcAGcATtGcTtGtTtGcGAGGgGcCCTTAATTTAAc 133
QY	381	ggaagctctgttccaatcccagcgtctcctcacagaanaaacctgtgcatgataaaaaaag 440
DB	132	GGAAGcTtTGTtCAATtCCAGcGgTcCTTAACAGAAAAGcCTGTGcATGAATAAAAAAG 73
QY	441	aagtttgttaatttatatacttttagtttagttatactaagattaaacatatttcgtata 500
DB	72	AAcTtTtGtRAATtTtATtATtAcTtTtTAGTtATtACTAAGTATtTAAACATtATTTcGTGA 13

QY	501	ttcttccaanaa 512		
Db	12	TTCTTCACACAA 1		
RESULT	14	AA455042	427 bp	mRNA
LOCUS	AA455042/c	aa04a07.s1 Soares.NHMPU_S1	Homo sapiens	linear EST 06-JUN-1997
DEFINITION	3', mRNA sequence.			IMAGE:812244
ACCESSION	AA455042			
VERSION	AA455042.1	GI:2177818		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
AUTHORS	1 (bases 1 to 427)			
	Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisler,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,T., Moore,B., 'T., Matternberg,K., Steppe,M., Tan,F., Theisling,B., White,Y., Wyllie , Schellenberg,R., and Wilson.R.			
TITLE	WashU-Merck EST Project 1997			
JOURNAL	Unpublished (1997)			
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m3 fwd. ER from Amersham High quality sequence stop: 395. Location/Qualifiers 1..427 /organism="Homo sapiens" /db_xref="GDB:6043155" /db_xref="taxon:9606" /clone="IMAGE:812244" /clone_lib="Soares_NHMPU_S1" /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH10B" /note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBH19M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."			
BASE COUNT	119 a	101 c	91 g	116 t
ORIGIN				
Query Match	80.0%;	Score 427;	DB 9;	Length 427;
Best Local Similarity	100.0%;	Pred. No. 5,6e-51;		
Matches 427;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	81	tcgcagaaccctaccacgcagcagcagctgagagaggttgagggaagtgcctgctgaggt 140		
Db	427	TCGCAGAACTACTCAGGCGACCCAGCTGAGAGAGGTTGAGGGAAGTGCCTGCTGGGT 368		
QY	141	ctgcagacgcgagatggataacgctgcagcgcggaataaacaatcgccctctgcttcagtg 200		
Db	367	CTGCAGACGCAGTGGATTAACGTGACGCGGAATAATTAACAATTCGCCCTTGTGCTTCAAGTG 308		
QY	201	tgaagagccacggtgaagaatgctgcgctgtagatattatcaactcaactcgtgtgaacaacagtat 260		

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|||||
Db 307 TGAAGGCCACGGAAGATGCTGGCTGGATATATCACTGATGATACACAGTAT 248
Oy 261 tcatgctcatcgtatctgtgttgcaactgataccagaacacaacatgacgtgtg 320
Db 247 TATGCTCATCGTATCTGTGTGGCACTGATACAGAAACACAACTGACAGTTGGTG 188
Oy 321 gagggtgtgttgcaactgtgtgacagagatgtgtctgtgcagaggggccttattac 380
Db 187 GAGGGGTGTGTGACATGTGTGACACAGTATGCTGTTCGCCAGCGGGGCCCTTATTACC 128
Oy 381 ggaagcttctgttcaatccagcaggtcttaccagaagaaagcctgtgcaagaaaaaag 440
Db 127 GGAAGCTTCTGTCAATCCACAGCGTCTTACCAAGAAAGCCTGTGATGAAAAAG 68
Oy 441 aagcttctgttcaatcttattactttagttgatactaaagtataaatacttctgta 500
Db 67 AAGTTTGTATTTTATATTAATCTTTTGTGATTAAGTATTAACATATTTCTGTA 8
Oy 501 ttcttcc 507
Db 7 TTCTTCC 1

RESULT 15
A1128804 423 bp mRNA linear EST 05-OCT-1998
LOCUS q94b08.s1 Soares_fetal_heart_NbHL19w Homo sapiens cDNA clone
DEFINITION IMAGE:1694391 3', mRNA sequence.
ACCESSION A1128804
VERSION A1128804.1 GI:3597318
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ccgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 382 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 413.
location/Qualifiers
    1..423
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:1694391"
    /clone_lib="Soares_fetal_heart_NbHL19w"
    /sex="unknown"
    /dev_stage="19 weeks"
    /lab_host="DH10B (ampicillin resistant)"
    /note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCCGATCTTTTGTGTGTGTGT 3'], RI
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Col - 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19w."
BASE COUNT 116 a 101 c 89 g 117 t
ORIGIN

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Query Match 79.0%; Score 422; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 2,8e-50;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 82 cgcgaacctactcagcagccagctgagaagatgagggaaagtgcgtcgtggtc 141
Db 423 CGCAGAACCTACTCAGCGACGCGCTGAGAGAGTGGAGGAAAGTCCTGCTGGGTC 364
Oy 142 tgcagacgcgatgagtaacgtgtcagccggaataaacaacgccttctgtcagct 201
Db 363 TGCAGACCGGATGGATTAACGTCACGCCGAAATTAACATCGCCCTTCTGCTCACTGT 304
Oy 202 gaaagccacgtgaagatgctgcygctggatataatcaactcactgylaaacagatc 261
Db 303 GAAAGCCACGTAAGATGCTCGGCTGGATATTAATCAACTCACTGGTAACAACAGTAT 244
Oy 262 catgctcatcgtatctgtgttgcaactgtatccagaacacacacttgcaagttgtg 321
Db 243 CATGCTCATCGTATCTGTGTGGCACTGATACCAAGAACCAACACATTAAGTGTGG 184
Oy 322 aggggtgttgcaactgtgacagcaatgctgtcttgcagaggggccttattaccg 381
Db 183 AGGGGTGTGTGCACTTGTGACACAGCACTATGCTGTTCGCCAGCGGGCCCTTATTACCG 124
Oy 382 gaagcttctgttcaatccagcaggtcttaccagaagaaagcctgtgcaagaaaaaaga 441
Db 123 GAAGCTTCTGTCAATCCACAGCGTCTTACCAAGAAAGCCTGTGATGAAAAAGAA 64
Oy 442 agtttgaatttattactttagttgatactaaagtataaatacttctgta 501
Db 63 AGTTTGTATTTTATATTAATCTTTTGTGATTAAGTATTAACATATTTCTGTAT 4
Oy 502 tc 503
Db 3 TC 2

Search completed: July 17, 2002, 08:47:42
Job time: 9817 sec

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